

GenCore version 4.5  
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OK protein - protein search, using sw model

Run on: October 12, 2001, 16:09:03 ; Search time 22.7 Seconds  
(without alignments)  
1812.637 Million cell updates/sec

Title: US-09-265-540E-2  
Perfect score: 1627  
Sequence: 1 MDTFTVLEIEITSLTFMWF.....VDACATAVMSPEELLRAWIS 311

Scoring table: BIOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 425026 seqs, 132305027 residues  
Total number of hits satisfying chosen parameters: 425026

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database :  
1: SPTRMBL\_16:\*  
2: sp\_archaea:\*  
3: sp\_bacteria:\*  
4: sp\_fungi:\*  
5: sp\_human:\*  
6: sp\_invertebrate:\*  
7: sp\_mammal:\*  
8: sp\_mmc:\*  
9: sp\_organellae:\*  
10: sp\_phage:\*  
11: sp\_plant:\*  
12: sp\_rhodent:\*  
13: sp\_unclassified:\*  
14: sp\_vertebrate:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|-------|-------------|--------|----|-------------|
| 1          | 202   | 12.4        | 569    | 13 | Q9YHWO      |
| 2          | 171.5 | 10.5        | 442    | 13 | Q9PVJ9      |
| 3          | 166.5 | 10.2        | 341    | 13 | Q9YGC8      |
| 4          | 157   | 9.6         | 332    | 11 | Q63953      |
| 5          | 153.5 | 9.4         | 308    | 13 | Q9PVK0      |
| 6          | 150.5 | 9.3         | 508    | 13 | Q9YHV9      |
| 7          | 138   | 8.5         | 553    | 4  | Q9UHF4      |
| 8          | 115   | 7.1         | 298    | 4  | Q9HD97      |
| 9          | 113   | 6.9         | 301    | 4  | Q95100      |
| 10         | 110.5 | 6.8         | 299    | 4  | Q9UBK4      |
| 11         | 108.5 | 6.7         | 292    | 4  | Q9UGN4      |
| 12         | 105.5 | 6.5         | 339    | 6  | Q9GK86      |
| 13         | 101.5 | 6.2         | 509    | 6  | Q9MYZ9      |
| 14         | 100.5 | 6.2         | 419    | 10 | Q9M0H3      |
| 15         | 98.5  | 6.1         | 484    | 4  | Q14936      |
| 16         | 97.5  | 6.0         | 229    | 6  | Q27950      |
| 17         | 95.5  | 5.9         | 229    | 6  | Q28206      |
| 18         | 95.5  | 5.9         | 1427   | 13 | Q91562      |
| 19         | 95    | 5.8         | 1445   | 11 | Q63155      |

|    |      |     |      |    |        |                    |
|----|------|-----|------|----|--------|--------------------|
| 20 | 92.5 | 5.7 | 666  | 13 | Q73876 | 073876 brachydanio |
| 21 | 92.5 | 5.7 | 1118 | 4  | Q15426 | Q15426 homo sapien |
| 22 | 92   | 5.7 | 422  | 4  | Q9UHM5 | Q9UHM5 homo sapien |
| 23 | 91.5 | 5.6 | 987  | 13 | Q73875 | Q73875 brachydanio |
| 24 | 91.5 | 5.6 | 1115 | 4  | Q9HD43 | Q9HD43 homo sapien |
| 25 | 91   | 5.6 | 422  | 4  | Q75462 | Q75462 homo sapien |
| 26 | 91   | 5.6 | 425  | 11 | Q9JMS8 | Q9JMS8 mus musculu |
| 27 | 88   | 5.4 | 1527 | 11 | Q9ES67 | Q9ES67 rattus norv |
| 28 | 87.5 | 5.4 | 227  | 8  | Q9G3S0 | Q9G3S0 challoolobu |
| 29 | 87.5 | 5.4 | 1274 | 3  | Q9UN05 | Q9UN05 schizosach  |
| 30 | 87   | 5.3 | 896  | 11 | Q64146 | Q64146 rattus norv |
| 31 | 86   | 5.3 | 227  | 8  | Q37596 | Q37596 phyllostomu |
| 32 | 86   | 5.3 | 227  | 8  | Q9G390 | Q9G390 echinops te |
| 33 | 86   | 5.3 | 228  | 8  | Q9ML06 | Q9ML06 limulus pol |
| 34 | 86   | 5.3 | 495  | 2  | Q34660 | Q34660 bacillus su |
| 35 | 85.5 | 5.3 | 1647 | 5  | Q9YVW1 | Q9YVW1 dtrosophila |
| 36 | 85   | 5.2 | 227  | 8  | Q9G947 | Q9G947 protilhecus |
| 37 | 85   | 5.2 | 592  | 4  | Q95697 | Q95697 homo sapien |
| 38 | 85   | 5.2 | 1294 | 4  | Q9UQP3 | Q9UQP3 homo sapien |
| 39 | 84.5 | 5.2 | 345  | 5  | P91030 | P91030 caenorhabdi |
| 40 | 84.5 | 5.2 | 752  | 1  | Q9YCG1 | Q9YCG1 aeropyrum p |
| 41 | 84.5 | 5.2 | 1252 | 11 | Q9ECS9 | Q9ECS9 mus musculu |
| 42 | 84   | 5.2 | 227  | 8  | Q9MET3 | Q9MET3 pyseater ca |
| 43 | 84   | 5.2 | 227  | 8  | Q9G6N2 | Q9G6N2 pteropus da |
| 44 | 84   | 5.2 | 2297 | 3  | Q9HGK6 | Q9HGK6 candida alb |
| 45 | 83.5 | 5.1 | 220  | 8  | Q9XN00 | Q9XN00 stomaphis a |

## ALIGNMENTS

RESULT 1  
ID Q9YHWO PRELIMINARY: PRT: 569 AA.  
AC Q9YHWO;  
DT 01-MAY-1999 (TREMBLrel. 10, Created)  
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)  
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
DE INTERFERON ALPHA/BETA RECEPTOR 1.  
GN IFNARI.  
OS Gallus gallus (Chicken).  
OC Eukaryota; Metazoa; Chordata; Cranata; Vertebrata; Euteleostomi;  
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;  
OC Gallus.  
OX NCBI\_TaxID=9031;  
RN [1]  
RP SEQUENCE FROM N.A.  
RC TISSUE=LIVER;  
RA Rebol J., Gardiner K., Monneron D., Uze G., Lutfalla G.;  
RT \*Comparative genomic analysis of the Interferon/Interleukin-10  
RT Receptor gene cluster\*;  
RL Genome Res. 0:0-0(1999).  
DR EMBL: AF082664; AADI369.1; -;  
DR InterPro: IPR000282; -;  
DR InterPro: IPR001777; -;  
DR Pfam: PF00041; fn3; 1.  
KW SMART: SM00060; FN3; 1.  
KW Receptor.  
SQ SEQUENCE 569 AA; 64055 MW; 6A757DDEB891E605 CRC64;

Query Match 12.4%; Score 202; DB 13; Length 569;  
Best Local Similarity 25.2%; Pred. NO. 1.1e-10;  
Matches 79; Conservative 50; Mismatches 127; Indels 58; Gaps 14;  
QY 21 YALIPCL-LTDEVALPAPONLSVLTNNKHLMSFVIAPGETVYVSVEY-QGEYESLY 78  
DB 222 FSDIHCKITRKVNDLCPNVRFAALNMFYLLMDNHY--NEHVYTVQVLTITKLY 279  
QY 79 T--SHWIPSSWCSLTGEPEDVTDITAT-VPYNLVRATLGSOTSAWS----- 125  
DB 280 DDVSSKNQKVSCGENTISMKCNLSIVIKPTISASYFRVQANNEYSKSCLSDVEVDPPVT 339

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OY 126 -----ILKHPENRNSITLRPGMEIKKXGFHVLIELEDGPOFEFLVAYWX 171
DB 340 NEIGPPPVKVDISDYLH-----IKITPG-----GPGNKIMSDLYD-----FSYQILYWK 385
OY 172 REPGAEEHVAKMNSGGIPVHLETPMGAAVCVKAOTFVKALGXSAFSQTECV- EVGGEA 230
DB 386 NSSDNEEVKMKETKQIATVSDIAPSTLYCVKQVAFSEAYKNSDSFRECIGTAGGKH 445
OY 231 IPIVLAFVAVGFLLIIVVP-----LFWMKGRLLQYSCCPVVVLPDTL-----KITNSP 281
DB 446 LPLIT-LATFGALTVVLIVASLVIFELYOVNKKIKYMFPSQCPPLNIEGFGALFSSP 504
OY 282 OKLISCRREVDAC 295
DB 505 --FVPTVEEPPEIC 516

RESULT 2
O9PVJ9 PRELIMINARY; PRT; 442 AA.
O9PVJ9;
O1-MAY-2000 (Tremblrel. 13, Created)
O1-MAY-2000 (Tremblrel. 13, Last sequence update)
O1-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 1 (FRAGMENT).
GN IFNARI.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RX SEQUENCE FROM N.A.
RA Rebol J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the Interferon/Interleukin-10
receptor gene cluster."
RL Genome Res. 9:242-250(1999).
DR EMBL: AF082667; AAD13679.1; -.
DR InterPro: IPR001777; -.
DR Pfam: PF00041; fn3; 1.
DR SMART: SM00060; FN3; 1.
KW Receptor.
FT NON_TER
SQ SEQUENCE 442 AA; 49877 MW; 839EBE92170609E0 CRC64;

Query Match 10.5%; Score 171.5; DB 13; Length 442;
Best Local Similarity 27.0%; Pred. No. 5.8e-08;
Matches 64; Conservative 29; Mismatches 99; Indels 45; Gaps 9;
OY 21 YALPCL-LTDEVALTPAPONLSVSTNMKHLMMSPVIAFGTEVYVSVEY-OGEEYESLY 78
DB 222 FSPHCHIKTRKRVNLDLCPTVRFALNMKFYLLMDNHY--NEHYTTVOVLITGLKMLY 279
OY 79 T--SHIWPSSWCSLTGEGPCDVTDDITAT--VPYNLRVRAIIGSOTSAMS----- 125
DB 280 DDVSSKMQKSGCENITSMKCNLSVYKPTSAHYFRQANNEYKNSCLSKDVEVDPPVT 339
OY 126 -----ILKHPFRNSTIILTRPGMEIKKXGFHVLIELEDGPOFEFLVAYWX 171
DB 340 NEIGPPPVKVDISDYLH-----IKITPG-----GPGNKIMSDLYD-----FSYQILYWK 385
OY 172 REPGAEEHVAKMNSGGIPVHLETPMGAAVCVKAOTFVKALGXSAFSQTECVG 228
DB 386 NSSDNEEVKMKETKQIATVSDIAPSTLYCVKQVAFSEAYKNSDSFRECIGTAG 442

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DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERLEUKIN-10 RECEPTOR 2.
GN IL10R2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RX SEQUENCE FROM N.A.
RA Rebol J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the Interferon/Interleukin-10
receptor gene cluster."
RL Genome Res. 0:0-0(1999).
DR EMBL: AF082667; AAD13678.1; -.
DR EMBL: AF082666; AAD13671.1; -.
DR HSSP: P13726; 2HRT.
DR InterPro: IPR000282; -.
DR InterPro: IPR001187; -.
DR InterPro: IPR001777; -.
DR Pfam: PF00041; fn3; 1.
DR PRINTS: PR00346; TISSUEFACTOR.
DR SMART: SM00060; FN3; 1.
KW Receptor.
SQ SEQUENCE 341 AA; 39062 MW; 18027239BF8A9C87 CRC64;

Query Match 10.2%; Score 166.5; DB 13; Length 341;
Best Local Similarity 21.2%; Pred. No. 1.2e-07;
Matches 62; Conservative 55; Mismatches 119; Indels 57; Gaps 12;
OY 22 ALIPLCLTDEVALTPAPONLSVSTNMKHLMMSPVIAFGTEVYVSVEYOGEEYESLYTSH 81
DB 8 ALMGLCLLCVSGIIVKPRNARISVNFBSVLLMDPGVKNISTVQ-----AKS 58
OY 82 IWPSSWCSLTGEGPCDVTDDITATVPYNLRVRAIIGSOTSAMSILKHPFRNSTIL 138
DB 59 IFPKQNFNNVTNLNLTVECDVS-SLSVGYAVLVRVTEMEDESDMAVYRFP-PMDVTYI 116
OY 139 TRPGMEIKKXGFHVLIELEDGPOFE-----FLVAYMKREGAEEHVAKM 182
DB 117 GPPSVNVKSESGLTHVDF--TGPAADREHDKMSLKQYGSMTYRILYMKK--GSNKKV-- 170
OY 183 VNSGGIPVHLET-----MEPGAAYCVKAOTFVKALGXSAFSQTECVGEGAI-P 232
DB 171 -----IHIDKHNSEILSQLEPWTITICIQYQGVLPENMKTGERSQELCEQTTNGVTP 223
OY 233 LVIALFAVGFML-ILVVVPL--FVWMKGRLLQYSCCPVVVLPDTLKITNSP 281
DB 224 WIVVTVLLGSMIAVIVSVPCFFAFWVLYRFTKHVFPFSYIFPOLKREFFSP 276

RESULT 4
O63953 PRELIMINARY; PRT; 332 AA.
O63953;
O1-NOV-1996 (Tremblrel. 01, Created)
O1-NOV-1996 (Tremblrel. 01, Last sequence update)
O1-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERFERON GAMMA RECEPTOR 2 (INTERFERON GAMMA RECEPTOR BETA SUBUNIT).
GN IFNGR2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RX SEQUENCE FROM N.A.
RA Hemmi S., Bohni R., Stark G., Di Marco F., Aguet M.;
RT "A novel member of the interferon receptor family complements
functionality of the murine interferon gamma receptor in human

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RT cells."
RN Cell 76:803-810(1994).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-129SV/7;
RX MEDLINE-97128072; PubMed-8972742;
RA Ebersperger C., Rhee S., Muthukumaran G., Lembo D., Donnelly R.,
RA Pestka S., Dambic Z.;
RT "Genomic organization and promoter analysis of the gene ifngt2
RT encoding the second chain of the mouse interferon-gamma receptor.";
RL Scand. J. Immunol. 44:599-606(1996).
DR EMBL; 069599; AAC52938.1; JOINED.
DR EMBL; 069594; AAC52938.1; JOINED.
DR EMBL; 069595; AAC52938.1; JOINED.
DR EMBL; 069596; AAC52938.1; JOINED.
DR EMBL; 069597; AAC52938.1; JOINED.
DR EMBL; 069598; AAC52938.1; JOINED.
DR EMBL; 569336; AAB30165.1; -.
DR MGD; MGI:107654; Ifngt2.
DR InterPro: IPR000282; -.
DR Pfam: PF00041; fn3; 1.
DR SMART; SM00060; FN3; 1.
SQ SEQUENCE 332 AA; 37471 MW; E2DD53BF934BA087 CRC64;

Query Match 9.6%; Score 157; DB 11; Length 332;
Best Local Similarity 27.0%; Pred. No. 9.5e-07;
Matches 72; Conservative 34; Mismatches 101; Indels 60; Gaps 17;

QY 17 MWFYALIPCLL-----TDEVALIPAPQNLSTNKKHLMSPVIAPEGTVYY 66
DB 6 LW-----LPSLLCGLGAASPSQSLAPLNPRLHLYNDEQILTWEP--SPSSNDR 58
QY 67 SVEYGEESLTSHTWIPSSWCSLTEGPEC-DVTD---DITA-----TYPYN--LKY 113
DB 59 PAVYGVES-----FLDGSWHRLLE-PNCTDITETKCDLGGGRLKLPFPFTVFLRY 110
QY 114 RATLSGTSAMSILKHPFNRSITLTPR--GMEIKKXGFHLYTELE---DL--GPOFEFL 166
DB 111 RAKRNLTSKMWGLE-PROHTENVYGPPEKNISVTPGKSLVHSPPEVDHEGATFYH 169
QY 167 VAYWXRPGAEEHVK--MYRSGGIPVHLETMEPGAAYCVKAQTFV---KAIGYSAFSQT 221
DB 170 VHYWKSSEYQEQVSGPFPSSNSIV--LGNLKYRYCYCQTEQGLIKNNKIRHGLLSNV 227
QY 222 ECVEVQGEA-----IPVLALFAFV 241
DB 228 SCHETTANASARLQGVILPIGLIFALL 254

RESULT 5
Q9PVK0 PRELIMINARY; PRT; 508 AA.
AC Q9PVK0;
DT 01-MAY-2000 (Tremblrel. 13, Created)
DT 01-MAY-2000 (Tremblrel. 13, Last sequence update)
DT 01-MAR-2001 (Tremblrel. 16, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 2.
GN IFNAR2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99177346; PubMed-10077530;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster.";
RL Genome Res. 9:242-250(1999).
DR EMBL; AF082667; AAD13677.1; -.

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DR HSSP; P24055; 1A21.
DR InterPro: IPR000282; -.
DR InterPro: IPR000342; -.
DR InterPro: IPR001187; -.
DR InterPro: IPR002048; -.
DR Pfam: PF01108; Tissue_fac; 1.
DR PRINTS; PR00346; TISSUEFACTOR.
DR ProDom; PD001580; -. 1.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 508 AA; 57175 MW; 4C02D29D243E8C05 CRC64;

Query Match 9.4%; Score 153.5; DB 13; Length 508;
Best Local Similarity 24.7%; Pred. No. 3.4e-06;
Matches 73; Conservative 46; Mismatches 116; Indels 61; Gaps 16;

QY 20 FYALI-----PCL-LTDEVALIPAPQNLSTNKKHLMSPVIAPEGTVYSVEY 70
DB 11 FYQLVFSILCAACYSLSSEKIPREP-PDNLQMTSNMFQHTLSWRASDPTVPTVRY-- 67
QY 71 QGEYESLTSHTI-WIPSSWCSLTEGPECQVTDI-TATVYNLAVKATIGQTSAMSL- 127
DB 68 -----LYSSHSMWKIAQCSRIYQPCNLTDDQVYVDSFSAFVQSFGEVENSSILY 121
QY 128 -----KHPFNRSITI-----LTPRGMEIKKXGFHLYTELEDLGPOFEFLVYWX 171
DB 122 FSPLSERFLCPPEPNNLSSCHVCHITITKLPPTHLRKNG--KLTLFDIYNKVNVEIT--L 177
QY 172 RPGAEEHVK--MYRSGGIPVHLETMEPGAAYCVKAQTFVKAIGXSAFSQTECEVQG 228
DB 178 RTVG-EERKSRSEKVEEPEPSIVELYPNRNCVSVWV-TASLNKHSIPAMKCTTDS 235
QY 229 EA-----IPVLALFAFVGMILVYVPLFVWKMGLLQYSCCPVYVLPFLKIT 278
DB 236 VAEKDYGYGITAVA---ICFSILVYLKCLHGLGYILNRKS-----LPDILVET 282

RESULT 6
Q9YHV9 PRELIMINARY; PRT; 508 AA.
ID Q9YHV9;
AC Q9YHV9;
DT 01-MAY-1999 (Tremblrel. 10, Created)
DT 01-MAY-1999 (Tremblrel. 10, Last sequence update)
DT 01-OCT-2000 (Tremblrel. 15, Last annotation update)
DE INTERFERON ALPHA/BETA RECEPTOR 2.
GN IFNAR2.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-LIVER;
RA Reboul J., Gardiner K., Monneron D., Uze G., Lutfalla G.;
RT "Comparative genomic analysis of the interferon/interleukin-10
RT receptor gene cluster.";
RL Genome Res. 0:0-0(1999).
DR EMBL; AF082665; AAD13670.1; -.
DR HSSP; P24055; 1A21.
DR InterPro: IPR000282; -.
DR InterPro: IPR001187; -.
DR InterPro: IPR002048; -.
DR Pfam: PF01108; Tissue_fac; 1.
DR PRINTS; PR00346; TISSUEFACTOR.
DR PROSITE; PS00018; EF_HAND; UNKNOWN_1.
KW Receptor.
SQ SEQUENCE 508 AA; 57049 MW; 5CE6DFED970DFB90 CRC64;

Query Match 9.3%; Score 150.5; DB 13; Length 508;
Best Local Similarity 24.3%; Pred. No. 6.0e-06;

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Matches 71; Conservative 46; Mismatches 122; Indels 53; Gaps 15;

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OY 20 FYALI-----PCL--LTDEVALPAPONLSVLTNNKHLIMSPVIAPEYVSYEV 70
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 11 FYOLVFIILCAACYSISLSEKIPREP--PDNLQMTSNNOHILSNRAHSDPVPVYRYV-- 67
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 71 QGEVESLYTSHI-WIPSSWCSLTGEPEDVTDIT-TATVPNLRATLGSOTSAMSLK 128
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 68 -----LYSSHSMNKIKAQCSRIYQPCNLTDQVVSDEXSAFQSVGTEVENSSILH 121
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 129 H-----PNNRNTI-----LTRPGMEIKKXGFHLYIELEDGPGPEFLVATWX 171
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 122 FSPSLSEFLPPEPNLSVCVCHITITKLPTHLKKN--KLSLFDIYNKVNTEIT--L 177
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 172 REPGAEEHVK--MYRSGGIPVHEETMEPGAAYCVKQTFYKAIQXSAFSQTECEVO- 227
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 178 RTVG-EEHKRSPEKYTEPEFSIVIEELYPNNKCVSMV--TASLKNKHSIPAMKITTDS 235
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
    228 -GEAIPVLAFAVGFLLIVVPLFVYKMGRLQYSCCVVVLDPPLKTT 278
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
    236 VAEKDYGYITAGAIQCSILVILKCLHGLGILHKRS-----LPDYLFT 282
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

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## RESULT 7

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ID 09UHF4 PRELIMINARY; PRT; 553 AA.
AC 09UHF4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)
DE CLASS II CYTOKINE RECEPTOR ZCYTOR7.
GN ZCYTOR7.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RA [1]
RP SEQUENCE FROM N.A.
RA Lok S., Kho C., Jelmberg A., Adams R., Whitmore T., Farrah T.,
RA O'Hara P.;
RT "Homo sapiens cytokine receptor homolog.":
RL Submitted (OCT-1999) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE FROM N.A.
RA Presnell S., Gilbert T., Whitmore T., Foster D., Hart C., Lehner J.,
RA Martinez T., Hoffman R., O'Hara P.;
RL Submitted (SEP-1999) to the EMBL/GenBank/DBJ databases.
EMBL: AF184971; AAF01320.1; -.
HSSP: P13726; 1TFH.
DR InterPro: IPR000282; -.
KW Receptor.
SQ SOURCE 553 AA; 62553 MW; 7C23C8543B114659 CRC64;

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Query Match 8.5%; Score 138; DB 4; Length 553;  
 Best Local Similarity 21.3%; Pred. No. 0.00011;  
 Matches 55; Conservative 43; Mismatches 98; Indels 62; Gaps 11;

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OY 24 IPCLLTDEVALPAPONLSVLTNNKHLIMSPVIA--PGEVYVSYEVQGEVESLYTSHI 82
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 30 VPCVSGG-----LPRANITFSLINKKNVLOMTPEPGLOGVYVTVQI-----FTYGOK 80
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 83 WIPSSWCSLTGEPEDVTDIT-ATVPNLRATLGSOTSAM--SLIKHPFNRR----- 134
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 81 WLNKSECRNINRTYCDLSAETSDYEHQYAKVKAIMGTCKSKMAESGFYFLEIQIGRP 140
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 135 -----STILTRGMEIKKXGFHLYIELEDGPGPEFLVAY-----WAKPEG 175
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 141 EVALTTDEKSLISVLTAP-EKMKRNPEDELPSVMOOISNLTNYNSVLTNKTNSRTWSQ--C 197
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 176 AEEHVKNVRSIGIPVHEETMEPGAAYCVKQTFYKAIQXSAFSQTECEVOGE----- 229
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 198 VTNHTLV-----LTWLEPNLTLCVHVHESFVPGPPRRAPQSPSEKQCARLTKDOSSSEFK 248
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

OY 230 -----ALPVLALFAF 240  
 DB 249 AKIIFVYVLPISITVFLF 266

## RESULT 8

```

ID 09HD97 PRELIMINARY; PRT; 298 AA.
AC 09HD97;
DT 01-MAR-2001 (TREMBLrel. 16, Created)
DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CMRF35H.
GN CMRF35H.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RA [1]
RP SEQUENCE FROM N.A.
RA Clark G.J., Green B.J., Hart D.N.J.;
RT "The CMRF35H gene structure predicts for an independently expressed
RT member of an ITIM/ITAM pair of molecules localized to human chromosome
RT 17."
RL Submitted (AUG-1999) to the EMBL/GenBank/DBJ databases.
DR EMBL: AF176991; AAF89957.1; -.
DR EMBL: AF176985; AAF89957.1; JOINED.
DR EMBL: AF176986; AAF89957.1; JOINED.
DR EMBL: AF176987; AAF89957.1; JOINED.
DR EMBL: AF176988; AAF89957.1; JOINED.
DR EMBL: AF176989; AAF89957.1; JOINED.
DR EMBL: AF176990; AAF89957.1; JOINED.
SQ SEQUENCE 298 AA; 33230 MW; DB58C9104A33B4C3 CRC64;

```

Query Match 7.1%; Score 115; DB 4; Length 298;  
 Best Local Similarity 22.8%; Pred. No. 0.0076;  
 Matches 53; Conservative 27; Mismatches 90; Indels 62; Gaps 9;

```

OY 51 LLMNSP-----VIAPGETVYVSYEVQGEVESLYTSHIWPSSWCSLTGEPEDV 100
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 8 LLLWPGCFALSKCRTVAGPWSLSVQCPYQKEHRTL-----NKWY--RPPQIFLC 57
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 101 DDIITVVPNLRATLGSOTSAMSLIKHPFNRSSTILTRPGMEIKKXGFHLYIELEDIG 160
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 58 DKIVET-----KGSAGKRNGRVSIKSDPANISFTVIENTLE-----EDAG 98
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 161 PQEFLVAYWXR--EPGAEEHVKNVRSIGIPVHEETMEPGAAYCVKQTFYKAI----- 212
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 99 TYWCGVDTFMLRDHPDHPVVEVSVPPAS-----TSMTPASITAKTSTITTAFFPPVS 152
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
OY 213 -----GXYSASFQTECEVOGEAIPVLAFAVGFLLIVVPLFVYKMGRLQYSCCVV 257
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
DB 153 TTLFAVGATSHASIQETEEVVNSQPLLLSLAL--LLLVGASLLAMRM 202
    |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

```

## RESULT 9

```

ID 095100 PRELIMINARY; PRT; 301 AA.
AC 095100;
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE CMRF-35-H9.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX NCBI_TaxID=9606;
RA [1]
RP SEQUENCE FROM N.A.
RA Green B.J., Clark G.J., Hart D.N.J.;
RT "The CMRF-35 monoclonal antibody recognised a second leucocyte
```

[illegible]

```

Query Match 5.8%, Score 110.5; DB 4; Length 299;
Best Local Similarity 23.7%; Pred. No. 0.02;
Matches 55; Conservative 25; Mismatches 91; Indels 61; Gaps 10;

QY 51 LLMNSP-----VIAPEFTVYVSYEGEYSLYTSHTMIPSSWCSLTEGPCDVT 100
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 8 LLLWPGCFALSKCKTVAGP---VGSLSVQCPYEK---EHRTLKMYC---RPQIFLC 58

QY 101 DDITATVYVNLVRKATLSQTSAMSILKHPPFNRSITILTRQMETLKKXGFHLVLELDG 160
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 59 DKIVET-----KGSACKRNGRVSIRSPANLSFTVLENLTE-----EDAG 99

QY 161 PQEFELVAYWK---EPGAEHEHVKNVRSGGIPIVHLETPMEPGAAYCVKQATFYKAI----- 212
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 100 TYWCVCVDTFPMILDFHPDPVVEEVSFPAS-----TSMTPASITAKTSTTTAPPVSS 153

QY 213 -----GXSAFSQTECEVEOGEAIPVLALFAFVGFMILLVVPFLVWKM 257
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 154 TTLFAVGATHSASIQEETEEVYVNSQLPILLSLALL--LLLLVGASLLAMRW 203

RESULT 11
Q9UGN4 PRELIMINARY; PRT; 299 AA.
AC O9UGN4;
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2001 (TREMBLrel. 16, Last annotation update)
DE NK INHIBITORY RECEPTOR.
OS RC2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
NCBI_TaxID=9606;
[1]
RN RP SEQUENCE FROM N.A.
RC TISSUE-LYMPHOID;
RA Cantoni C., Blasson R.;
RL "Irp60 a novel NK inhibitory receptor."
RL Submitted (APR-1999) to the EMBL/Genbank/DBJ databases.
CC -1. SIMILARITY: TO IMMUNOGLOBULIN AND MAJOR HISTOCOMPATIBILITY COMPLEX DOMAIN.
CC EMBL; AJ238323; CAB66145.1; -.
DR InterPro; IPR003006; -.
DR InterPro; IPR003599; -.
DR Pfam; PF00047; Ig; 1.
DR SMART; SM00409; IG; 1.
KM Receptor.
SQ SEQUENCE 299 AA; 33172 MW; 3999B1D8563B63BB CRC64;

Query Match 6.7%; Score 108.5; DB 4; Length 299;
Best Local Similarity 23.0%; Pred. No. 0.031;
Matches 55; Conservative 23; Mismatches 86; Indels 75; Gaps 11;

QY 51 LLMNSP-----VIAPEFTVYVSYEGEYSLYTSHTMIPSSWCSLTEGPCDVT 100
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 8 LLLWPGCFALSKCKTVAGP---VGSLSVQCPYEK---EHRTLKMYC---RPQIFLC 58

QY 101 DDITATVYVNLVRKATLSQTSAMSILKHPPFNRSITILTRQMETLKKXGFHLVLELDG 160
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 59 DKIVET-----KGSACKRNGRVSIRSPANLSFTVLENLTE-----EDAG 99

QY 161 PQEFELVAYWK---XRPGEAEHEHVKNVRSGGIPIVHLETPMEPGAAYCVKQATFYKAI----- 210
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 100 -----TYWCVCVDTFPMILDFHPDPVVEEVSFPAS-----TSMTPASITAKTSTTT 146

QY 211 AI-----GXSAFSQTECEVEOGEAIPVLALFAFVGFMILLVVPFLVWKM 257
   ||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 147 AAFPVSSTTLFAVGATHSASIQEETEEVYVNSQLPILLSLALL--LLLLVGASLLAMRW 203

```

RESULT 12  
 ID 09GR86 PRELIMINARY; PRT: 332 AA.  
 AC 09GR86;  
 DT 01-MAR-2001 (TREMBLrel. 16, Created)  
 DT 01-MAR-2001 (TREMBLrel. 16, Last sequence update)  
 DE TYPE I INTERFERON RECEPTOR 1E.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidea;  
 OC Bovidae; Caprinae; Ovis.  
 NCBI\_TaxID=9940;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Han C., Roberts M.;  
 RT "Antiviral activity of interferon receptors."  
 RL Submitted (AUG-2000) to the EMBL/GenBank/DBJ databases.  
 EMBL: AF296666; AAG42376.1; -  
 RECEPTOR.  
 SEQUENCE 332 AA; 38095 MW; 2CE7B93EC44B0E09 CRC64;

Query Match 6.5%; Score 105.5; DB 6; Length 332;  
 Best Local Similarity 28.1%; Pred. No. 0.068;  
 Matches 34; Conservative 20; Mismatches 48; Indels 19; Gaps 5;

Y 21 YAIIPCLLTDEVALPAPONLSVLTSMKHLMSPIAPGETYYSVEYGEYESLYTS 80  
 ID 09MY29 PRELIMINARY; PRT: 509 AA.  
 AC 09MY29;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 ERYTHROPOIETIN RECEPTOR.  
 SUS scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,  
 RT Christensen R.K., Vallet J.L.;  
 RL "Porcine Erythropoietin Receptor: Molecular Cloning and Expression in  
 Embryonic and Fetal Liver."  
 RL Domestic. Anim. Endocrinol. 0:0-0(2000).  
 EMBL: AF274305; AAF77065.1; -  
 DR InterPro: IPR000572; -  
 DR InterPro: IPR001777; -  
 DR InterPro: IPR002996; -  
 DR InterPro: IPR003528; -  
 DR Pfam: PF00041; fn3; 1.  
 DR PROSITE: PS01352; HEMATOPO\_REC\_L\_F1; UNKNOWN\_1.  
 DR PROSITE: PS00559; MOLYBDOPTERIN\_EUK; UNKNOWN\_1.  
 DR SMART: SM00060; FN3; 1.  
 KW Receptor.  
 SO SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCDBA CRC64;

Y 21 YAIIPCLLTDEVALPAPONLSVLTSMKHLMSPIAPGETYYSVEYGEYESLYTS 80  
 ID 09MY29 PRELIMINARY; PRT: 509 AA.  
 AC 09MY29;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE 01-MAR-2001 (TREMBLrel. 16, Last annotation update)  
 ERYTHROPOIETIN RECEPTOR.  
 SUS scrofa (Pig).  
 OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Suidae; Sus.  
 NCBI\_TaxID=9823;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Pearson P.L., Smith T.P.L., Sonstegard T.S., Klemcke H.G.,  
 RT Christensen R.K., Vallet J.L.;  
 RL "Porcine Erythropoietin Receptor: Molecular Cloning and Expression in  
 Embryonic and Fetal Liver."  
 RL Domestic. Anim. Endocrinol. 0:0-0(2000).  
 EMBL: AF274305; AAF77065.1; -  
 DR InterPro: IPR000572; -  
 DR InterPro: IPR001777; -  
 DR InterPro: IPR002996; -  
 DR InterPro: IPR003528; -  
 DR Pfam: PF00041; fn3; 1.  
 DR PROSITE: PS01352; HEMATOPO\_REC\_L\_F1; UNKNOWN\_1.  
 DR PROSITE: PS00559; MOLYBDOPTERIN\_EUK; UNKNOWN\_1.  
 DR SMART: SM00060; FN3; 1.  
 KW Receptor.  
 SO SEQUENCE 509 AA; 55183 MW; 35B565D07C6BCDBA CRC64;

Query Match 6.2%; Score 101.5; DB 6; Length 509;  
 Best Local Similarity 24.0%; Pred. No. 0.28;  
 Matches 68; Conservative 44; Mismatches 102; Indels 69; Gaps 18;

Y 31 EVAILPA--PQNLVSLTNMKHL-MW-----SPVAPGETYYSVEYGEYSLSYSHW 83  
 ID 09MOH3 PRELIMINARY; PRT: 419 AA.  
 AC 09MOH3;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 HYPOTHELICAL 47.3 KDA PROTEIN.  
 GN ATG28580.  
 OS Arabidopsis thaliana (mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,  
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project.  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL161573; CAB81446.1; -  
 KW Hypothetical protein.  
 SO SEQUENCE 419 AA; 47250 MW; DEB4003B682FBECEB CRC64;

Query Match 6.2%; Score 100.5; DB 10; Length 419;  
 Best Local Similarity 20.2%; Pred. No. 0.27;  
 Matches 50; Conservative 45; Mismatches 88; Indels 65; Gaps 8;

Y 28 LTDEVALPAPONLS---VLTSMKHLMSPIAPGETYYSVEYGEYSLSYSHW 84  
 ID 09MOH3 PRELIMINARY; PRT: 419 AA.  
 AC 09MOH3;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 HYPOTHELICAL 47.3 KDA PROTEIN.  
 GN ATG28580.  
 OS Arabidopsis thaliana (mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,  
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project.  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL161573; CAB81446.1; -  
 KW Hypothetical protein.  
 SO SEQUENCE 419 AA; 47250 MW; DEB4003B682FBECEB CRC64;

Query Match 6.2%; Score 100.5; DB 10; Length 419;  
 Best Local Similarity 20.2%; Pred. No. 0.27;  
 Matches 50; Conservative 45; Mismatches 88; Indels 65; Gaps 8;

Y 28 LTDEVALPAPONLS---VLTSMKHLMSPIAPGETYYSVEYGEYSLSYSHW 84  
 ID 09MOH3 PRELIMINARY; PRT: 419 AA.  
 AC 09MOH3;  
 DT 01-OCT-2000 (TREMBLrel. 15, Created)  
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)  
 DE 01-OCT-2000 (TREMBLrel. 15, Last annotation update)  
 HYPOTHELICAL 47.3 KDA PROTEIN.  
 GN ATG28580.  
 OS Arabidopsis thaliana (mouse-ear cress).  
 OC Eukaryota; Viridiplantae; Embryophyta; Tracheophyta; Spermatophyta;  
 OC Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II;  
 OC Brassicales; Brassicaceae; Arabidopsis.  
 NCBI\_TaxID=3702;  
 RX [1]  
 RP SEQUENCE FROM N.A.  
 RA Lennard N., Quail M., Harris B., Rajandream M.A., Barrell B.G.,  
 RA Mewes H.W., Lemcke K., Mayer K.F.X.;  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 RN [12]  
 RP SEQUENCE FROM N.A.  
 RA EU Arabidopsis sequencing project.  
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.  
 DR EMBL: AL161573; CAB81446.1; -  
 KW Hypothetical protein.  
 SO SEQUENCE 419 AA; 47250 MW; DEB4003B682FBECEB CRC64;







GenCore version 4.5  
Copyright (c) 1993 - 2000 Compugen Ltd.

OM protein - protein search, using sw model

Run on: October 12, 2001, 16:08:43 ; Search time 16 Seconds

(without alignments)  
1480.643 Million cell updates/sec

Title: US-09-265-540E-2

Perfect score: 1627

Sequence: 1 MDTFTVLEIEITWTSLEPMWF.....VDACATVMSPEILLRAMIS 311

Scoring table: BL0SUM62

Gapop 10.0 , Gapext 0.5

Searched: 219241 seqs, 76174552 residues

Maximum DB seq length: 0

Post-processing: Minimum Match 0%

Database : PIR\_68:\*

1: pir1:\*

2: pir2:\*

3: pir3:\*

4: pir4:\*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | DB ID    | Description         |
|------------|-------|-------------|--------|----------|---------------------|
| 1          | 191   | 11.7        | 325    | 2 A47003 | cytokine receptor   |
| 2          | 178.5 | 11.0        | 337    | 2 I38500 | interferon gamma r  |
| 3          | 178.5 | 11.0        | 590    | 2 A45283 | interferon alpha/b  |
| 4          | 175.5 | 10.8        | 349    | 2 JC6311 | interferon receptor |
| 5          | 164.5 | 10.1        | 560    | 2 S27387 | interferon alpha r  |
| 6          | 162.5 | 10.0        | 557    | 2 A32694 | interferon alpha/b  |
| 7          | 157   | 9.6         | 332    | 2 A49947 | interferon gamma r  |
| 8          | 136   | 8.4         | 578    | 2 I56215 | interleukin-10 rec  |
| 9          | 130   | 8.0         | 292    | 1 KFRB3  | tissue factor prec  |
| 10         | 125.5 | 7.7         | 295    | 1 KFRH3  | tissue factor prec  |
| 11         | 125.5 | 7.4         | 575    | 1 A49667 | tissue factor prec  |
| 12         | 121   | 7.4         | 489    | 2 A31555 | interleukin-10 rec  |
| 13         | 116.5 | 7.2         | 294    | 1 KEMS3  | tissue factor prec  |
| 14         | 114.5 | 7.0         | 292    | 1 KFRB3  | tissue factor prec  |
| 15         | 114   | 7.0         | 507    | 1 A32385 | erythropoietin rec  |
| 16         | 100.5 | 6.2         | 419    | 2 T10652 | hypothetical prote  |
| 17         | 99    | 6.1         | 507    | 1 A46713 | erythropoietin rec  |
| 18         | 97    | 6.0         | 508    | 1 ZUHR   | erythropoietin rec  |
| 19         | 96    | 5.9         | 984    | 2 A39753 | protein-tyrosine-p  |
| 20         | 95.5  | 5.9         | 1427   | 2 I51669 | tumor suppressor k  |
| 21         | 95    | 5.8         | 1447   | 2 A54100 | tumor suppressor p  |
| 22         | 92.5  | 5.7         | 987    | 2 A54092 | protein-tyrosine p  |
| 23         | 92.5  | 5.7         | 1118   | 1 A49724 | protein-tyrosine-p  |
| 24         | 89    | 5.5         | 831    | 2 J01655 | prolactin receptor  |
| 25         | 89    | 5.5         | 977    | 2 S49004 | tyrosine kinase Mp  |
| 26         | 88.5  | 5.4         | 1928   | 2 J50610 | beta-galactosidase  |
| 27         | 88    | 5.4         | 985    | 2 I51549 | erythropoietin rec  |
| 28         | 88    | 5.4         | 985    | 2 I51549 | receptor tyrosine   |
| 29         | 87.5  | 5.4         | 1274   | 2 T39249 | probable tripeptid  |

|    |      |     |      |          |                    |
|----|------|-----|------|----------|--------------------|
| 30 | 87   | 5.3 | 896  | 2 I56563 | interleukin-3 rece |
| 31 | 87   | 5.3 | 952  | 2 I50612 | protein-tyrosine k |
| 32 | 86   | 5.3 | 227  | 2 I37081 | cytochrome-c oxida |
| 33 | 86   | 5.3 | 327  | 2 T11483 | cytochrome-c oxida |
| 34 | 86   | 5.3 | 379  | 2 S56193 | probable membrane  |
| 35 | 86   | 5.3 | 495  | 2 H69614 | aldehyde dehydroge |
| 36 | 85.5 | 5.3 | 1557 | 2 D41214 | protein-tyrosine-p |
| 37 | 85.5 | 5.3 | 1630 | 2 C41214 | protein-tyrosine-p |
| 38 | 85   | 5.2 | 227  | 2 T11053 | cytochrome-c oxida |
| 39 | 85   | 5.2 | 227  | 2 T11250 | cytochrome-c oxida |
| 40 | 84.5 | 5.2 | 752  | 2 E72616 | hypothetical prote |
| 41 | 84   | 5.2 | 227  | 2 I61843 | cytochrome-c oxida |
| 42 | 84   | 5.2 | 227  | 2 T11860 | cytochrome-c oxida |
| 43 | 84   | 5.2 | 227  | 2 T11366 | cytochrome-c oxida |
| 44 | 84   | 5.2 | 227  | 2 T11431 | cytochrome-c oxida |
| 45 | 84   | 5.2 | 1482 | 2 S13495 | pregnancy zone pro |

## ALIGNMENTS

## RESULT 1

A47003

Cytokine receptor family class II protein CRF2-4 precursor - human

C:Species: Homo sapiens (man)

C:Date: 09-Sep-1994 #sequence\_revision 09-Sep-1994 #text\_change 01-Dec-2000

C:Accession: A47003; G01418

R:Infalila, G.; Gardiner, K.; Uze, G.

A:Title: A new member of the cytokine receptor gene family maps on chromosome 21 at 1

A:Reference number: A47003; M01D:93300510

A:Accession: A47003

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-325 <LUT>

A:Cross-references: GB:117227; NID:9393378; PIDN:CAA78933.1; PID:9393379

R:Infalila, G.

submitted to the EMBL Data Library, April 1994

A:Reference number: G06935

A:Accession: G01418

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-123, 'D', 125-268, 'VGRME' <LUT>

A:Cross-references: EMBL:008988; NID:9571295; PID:9571296

C:Genetics:

A:Gene: GDB:CRF4; CRF2-4

A:Cross-references: GDB:138168; OMIM:123889

A:Map position: 21q; 21q22.1-21q22.2

A:Introns: 17/1; 58/2; 111/1; 166/3; 216/1

C:Keywords: transmembrane protein

Query Match 11.7%; Score 191; DB 2; Length 325; Best Local Similarity 26.6%; Pred. No. 1.3e-09; Matches 77; Conservative 47; Mismatches 117; Indels 48; Gaps 16;

|    |     |  |
|----|-----|--|
| QY | 12  | WTSIFPMFFALICLTDEVAIIIPAPONLSVLTNKKHLIM-SPIYAPGETYYSVEY 70     |
| DB | 3   | W-SLGSW---LGGCLVSAAGWPPENRNVNFKNIQWSPAPAKG-----NLTF 52         |
| QY | 71  | QGESESYTHSIWIPSSMCSLTGECPCDVDDITATVPYNNRVARTLGSQTSAM-SILKH 129 |
| DB | 53  | TAQTLSTR-----IFDKCAMTTLTECDFS-SLSKYGDHILRVAREFADEHSDWNIIFC 106 |
| QY | 130 | PFNNSTILTRPGMEIKKXGFHLVIELEDLQPE-----FLVAYWKR 173              |
| DB | 107 | PV--DQILIPGKQGVLEADSL--HMRFLAPKLENEVETMTMKNVYSMTYVQW--K 160    |
| QY | 174 | PGAEHHKVMRSGGIPYHLETPGCAAYCYAKQFFVAIGXYSAFSQTECYE-VQGEAIP 232  |
| DB | 161 | NGTDEKFOITPOYDFEV-LRLLEPMTTYCYQVRRGLPDRNKAQMSSEVSCQTHDEIVP 219 |
| QY | 233 | ---LVALLFAFVGFNLLIVVPLF--VMKGRLLQYSCPPVYVLPDTLK 276            |

Db 220 SMWVAVILMASV-FMVCCLALGCFSLMCMCYKTKTKTAFSPRNLSPQHLLK 267

# RESULT 2

Interferon gamma receptor accessory factor-1 precursor - human

C:Species: Homo sapiens (man)

C:Date: 16-Feb-1996 #sequence, revision 16-Feb-1996 #text, change 05-Nov-1999

C:Accession: I38500; I38501

R:Sch, J.; Donnelly, R.J.; Kolenko, S.; Mariano, T.M.; Cook, J.R.; Wang, N.; Emanuel, S.

Cell 76, 793-802, 1994

A:Title: Identification and sequence of an accessory factor required for activation of

A:Reference number: A49946; MUID:94170380

A:Accession: I38500

A:Molecule type: mRNA

A:Residues: 1-337 <RES>

A:Cross-references: EMBL:U05875; NID:g463549; PIDN:AAAL6955.1; PID:g463550

A:Experimental source: clone pSKI

A:Accession: I38501

A:Molecule type: mRNA

A:Residues: 1-63, 'Q', 65-337 <RE2>

A:Cross-references: EMBL:U05877; NID:g463551; PIDN:AAAL6956.1; PID:g463552

A:Experimental source: clone pJS3

C:Genetics:

A:Map position: 21

C:Keywords: cytokine receptor

Query Match 11.0%; Score 178.5; DB 2; Length 337;

Best Local Similarity 26.1%; Pred. No. 1.8e-08;

Matches 75; Conservative 42; Mismatches 123; Indels 47; Gaps 14;

QY 11 IMTSLFMWFFYALIPCLTDEVALIPAPQNTSVLSTNKKHLLMSPVAPGET--VYYSV 68

Db 6 LMSLLLLGLVFAAAAAAPDPLSQLPAQHKIKLYNAEQVLSWEPVALMSNTRVYKRV 65

QY 69 EYQGEVSLYTSIMIDSSWCSLTREGPCDVTDITATVP-----YNLRVATLGS 119

Db 66 QFKYTDKMFADIMSIGVNCQTATATPC---DFTAASPAGFPMDFNVTLRLRAELGA 121

QY 120 QTSAMSLT---KHPFNNSITLTPRGMEIKKGFHLV-----ELEDLGQFQF-FLVAY 169

Db 122 LHSAMVTPMPFQH--YRNVTYGPPEMIEVTPREGSLIRFSSPDIAOTSTAFICYVHY 179

QY 170 WXPBPAGAEHYK-WYRSGGIPVHLETMEPGAAYCYKAKQ-----TFKAIQXGAFSOT 221

Db 180 W--EKGGIQVKGKPRNSIT--SLDNLKRPRVYCLQVQAQLMKNSNIFRPHLSNIS-- 233

QY 222 ECVFVGEA-IPVLALFAFYGMILIVVP---LFYMKGRLLQY 263

Db 234 -CYETMADASTELQOVILLISVGFSLSLVLAGACFVLVLRGLIKY 279

# RESULT 3

Interferon alpha/beta receptor - mouse

C:Species: Mus musculus (house mouse)

C:Date: 25-Mar-1993 #sequence, revision 18-Nov-1994 #text, change 05-Nov-1999

C:Accession: A45283; I48423; I48424; I48425; I48426; I48427; I48428; I48429

R:Uze, G.; Lutfalla, G.; Bandu, M.T.; Proudhon, D.; Mogensen, K.E.

Proc. Natl. Acad. Sci. U.S.A. 89, 4774-4778, 1992

A:Title: Behavior of a cloned murine interferon alpha/beta receptor expressed in homosp

A:Reference number: A45283; MUID:92265522

A:Accession: A45283

A:Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-590 <UZE>

A:Cross-references: GB:M89641; NID:g194111; PIDN:AAA37890.1; PID:g194112

A:Note: sequence extracted from NCBI backbone (NCBIN:102354, NCBIPI:102357)

R:lutfalla, G.; Uze, G.

Gene 148, 343-346, 1994

A:Title: Structure of the murine interferon alpha/beta receptor-encoding gene: high-freq

A:Reference number: I48423; MUID:95047447

A:Accession: I48423

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 118-125 <RES>

A:Cross-references: EMBL:U06337; NID:g497103; PIDN:AAA65003.1; PID:g755810

A:Accession: I48424

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 127-224 <RE2>

A:Cross-references: EMBL:U06238; NID:g497104; PIDN:AAAC01749.1; PID:g755811

A:Accession: I48425

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 243-264 <RE3>

A:Cross-references: EMBL:U06239; NID:g497106; PIDN:AAA65004.1; PID:g510261

A:Accession: I48426

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 265-375 <RE4>

A:Cross-references: EMBL:U06240; NID:g497108; PIDN:AAA65005.1; PID:g510262

A:Accession: I48427

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 397-424 <RE5>

A:Cross-references: EMBL:U06241; NID:g497110; PIDN:AAA65006.1; PID:g755812

A:Accession: I48428

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 426-445 <RE6>

A:Cross-references: EMBL:U06242; NID:g497112; PIDN:AAA65007.1; PID:g755813

A:Accession: I48429

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 473-590 <RE7>

A:Cross-references: EMBL:U06244; NID:g497114; PIDN:AAA65008.1; PID:g510265

C:Genetics:

A:Gene: IFNAR

A:Introns: 177/3; 331/1

C:Keywords: cytokine receptor; transmembrane protein

Query Match 11.0%; Score 178.5; DB 2; Length 590;

Best Local Similarity 23.0%; Pred. No. 3.6e-08;

Matches 76; Conservative 63; Mismatches 163; Indels 29; Gaps 13;

QY 3 TETMVLLEIMTSLFMWFFYALIPCLTDEVALIPAPQNTSVLSTNKKHLLMSPVAPGE 62

Db 197 TYCLEVKAIPHSLKHSNSTVOCISTVANKMPVGNLQVDAQGSYVLKMD-VLASAD 255

QY 63 TVYYSVEYQGEVSLTYTSHI--WIPSSWCSLTREGPCDVTDITATVPYNLRVATLGSQ 120

Db 256 VLFRAQWLPGYKSSSSGSHSDKKKPIPCANNOVTHICVSDQIVYVYGTFFLHQASBGNH 315

QY 121 TSAMSLIKHPFNNSITLTPRGMEIKKGFHLVIEL--EDLGPQFELVAYVXREPGEAE 177

Db 316 TSFWSSEKFLDSQKHILPPPVITVAMSDTLVLYVNCQDSTCDGLNYEIIFFW--EWTSN 373

QY 178 ENHKWYRSGGIPVHLETMEPGAAYCYKAKQTFVNA-IGXYSASFQOTCEVQGEAIPVLVA 236

Db 374 TISMEDKDP-EFTLNLQPLTYQVQARVLFALNLKTSNFSEKLECKERPQSFSTIWI 432

QY 237 LPAF-VGFMILIVVPL-LFYMKGRLLQYSCCPVVVLPTLKL--ITNSPOK--LISCR 289

Db 433 ITGLGVFFSVNVLALRSYWK---YLCHVCFPLPAPPSIDFSPSPSKNVLITLAE 489

QY 290 -----EVDACATAVM-SPELLRAWIS 311

Db 490 HIERCTIINTDPAVAEVKHAPEDELRKYS 520

# RESULT 4

JC6311

Interferon receptor-class II cytokine receptor - mouse

C:Species: Mus musculus (house mouse)

C>Date: 16-Jul-1999 #sequence\_revision 16-Jul-1999 #text\_change 11-May-2000

C:Accession: J06311

R:Gibbs, V.C.; Pennica, D.

Gene 186, 97-101, 1997

A:Title: cCRF2-4: Isolation of cDNA clones encoding the human and mouse proteins.

A:Reference number: J06311; MUID:97199375

A:Accession: J06311

A:Status: Preliminary

A:Molecule type: mRNA

A:Residues: 1-349 <GIB>

A:Cross-references: GB:U53696

Query Match 10.8%; Score 175.5; DB 2; Length 349;

Best Local Similarity 23.7%; Pred. No. 3.5e-08;

Matches 68; Conservative 47; Mismatches 119; Indels 53; Gaps 13;

QY 23 LIPC-----LTDEVAIIIPAPONLSVLTNNKRLHLMSPVIAPGETVYVSVEYQGEY 74

1 MAPCVAGMLGGFLVAPALGMIPPEKVRNNSVNFKNILQMEVPAPFKMLTFQAQE-SY 59

QY 75 ESLTSHWITSSWCSLTGEGPCDVTDDITATVPYNLRVRLTGLSQTSAW-SILKHPNR 133

60 RS-FQDH-----CKRTASTQCDPS-HLSKGYDYTVRAELADHSEWVNTFCPV-- 108

QY 134 NSTILTRPGMEIXKXGPHLVLELDLGPQFE-----FLVAVXKRGPGAE 177

109 EDTIIGPEMQLAESL--ELRPSAPQIENEPETWLNKIDSWAYVQW--KNGTN 164

QY 178 EHVAVRSGGIPVHLEMEPGAAYCAVKAQTEFKAIGXYSAFSQTCEVEVOGE----- 229

165 EKFOVVSYPDSV-LRNLEPWTTCIQOQGFLLDONRGENSEPICERNGENDEITSMWY 223

QY 230 AIPLVALLFAVFGMLLVVPLFWKMGRLLOYSQCPVVLPTLTK 276

224 AIIILVSVLVVFLFLGCFV--LMLIYKTKRKHFRSGTSLPQHILK 267

RESULT 5

527387

Interferon alpha receptor type 1 precursor - bovine

C:Species: Bos primigenius taurus (cattle)

C>Date: 13-Jan-1995 #sequence\_revision 13-Jan-1995 #text\_change 05-Nov-1999

C:Accession: S27387; S33770

R:Mouchel-Vielh, E.; Lutfalla, G.; Mogensen, K.E.; Uze, G.

FEBS Lett. 313, 255-259, 1992

A:Title: Specific antiviral activities of the human alpha interferons are determined at

Reference number: S27387; MUID:93076908

Accession: S27387

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-560 <MOU>

A:Cross-references: EMBL:X68443; NID:9431; PIDN:CAA48484.1; PID:g432

A:Experimental source: MDBK cells

R:Lim, J.K.; Langer, J.A.

Biochim. Biophys. Acta 1173, 314-319, 1993

A:Title: Cloning and characterization of a bovine alpha interferon receptor.

A:Reference number: S33770; MUID:93305725

A:Accession: S33770

A:Status: preliminary; nucleic acid sequence not shown

A:Molecule type: mRNA

A:Residues: 1-421, 'V', 423-560 <LIN>

A:Cross-references: EMBL:L06320; NID:9163187; PIDN:AAA02571.1; PID:g163188

A:Experimental source: Lung

C:Keywords: antiviral; cytokine receptor; transmembrane protein

F:1-24/Domain: signal sequence #status predicted <SIG>

F:25-560/Product: Interferon alpha receptor type 1 #status predicted <MAT>

Query Match

Best Local Similarity 10.1%; Score 164.5; DB 2; Length 560;

21.9%; Pred. No. 6.1e-07;

Matches 70; Conservative 62; Mismatches 136; Indels 51; Gaps 14;

QY 21 YALIPCLLTDEVALIPAPONLSVLTNNKRLHLMSPVIAPGETVYVSVEYQGEYESTLYTS 80

215 YSPYVCINTERRHKVSPENPQINADQIYLLKM-----DYENKNTFOQMLRAEFK 267

QY 81 HI-----W-IPSSWCSLTGEGPCDVTDDITATVPYNLRVRLTGLSQTSAWSILKHPF 131

268 KIPGNHSDKKWKOIFN--CENVTSTHCVFPPRVSRSRGIIYVVRASNGTSEFMSSEKFEFN 325

QY 132 NRNSTILTRPGM--ELIKXGFHLVI-----ELELDLGPQ-----PEFLVAVXKRGPGAEHV 180

326 TEKTTITFPPIVSVKSTYDLSHVSQASESEMSVNLPLIYETVLEMTSNAEKRY 385

QY 181 KIVRSGGIPVHLEMEPGAAYCAVKAQTEFVK--AIGXYSAFSQTCEVEVOGE-----GEAIPLV 234

386 LEKRTNTI---FPLKRLVYCVARALIEDNRKSSSFSDYCEKRPKPNSTWILY 442

QY 235 LALFAVGMILLVPLFWKMGRLLOYSQCPVVLPTLTK--ITNSPQR--LISCRRE 290

443 GTCTALFSIPVYIVVSVFL---RCVKYVFFPSKPPSSVDEYFSDQPLRNLILTSEE 498

QY 291 EVDAC-----ATAVMSPEE 304

499 QTERCFIENASITTEIEE 517

RESULT 6

A32694

Interferon alpha/beta receptor precursor - human

C:Species: Homo sapiens (man)

C>Date: 22-Jun-1990 #sequence\_revision 22-Jun-1990 #text\_change 22-Oct-1999

C:Accession: A32694; S17112

R:Uze, G.; Lutfalla, G.; Gresser, I.

Cell 60, 225-234, 1990

A:Title: Genetic transfer of a functional human interferon alpha receptor into mouse

A:Reference number: A32694; MUID:90124632

A:Accession: A32694

A:Molecule type: mRNA

A:Residues: 1-557 <UZE>

A:Cross-references: GB:003171; NID:g184645; PIDN:AAA52730.1; PID:g306914

R:Lutfalla, G.

A:Submitted to the EMBL Data Library, July 1991

A:Description: The structure of the human interferon alpha/beta receptor gene.

A:Reference number: S17112

A:Accession: S17112

A:Molecule type: DNA

A:Residues: 1-16, 'A', 18-329, 'V', 343-557 <LUT>

A:Cross-references: EMBL:X60459; NID:g32671

C:Genetics:

A:Gene: GDB:IFNAR1; IFNAR; IFRC

A:Cross-references: GDB:120078; OMIM:107450

A:Map position: 21q22.1-21q22.1

A:Introns: 26/1; 67/2; 126/1; 177/3; 225/1; 263/2; 342/1; 381/3; 432/1; 480/3

C:Keywords: cytokine receptor; glycoprotein; transmembrane protein

F:1-21/Domain: transmembrane #status predicted <TRM1>

F:437-455/Domain: transmembrane #status predicted <TRM2>

F:50,58,81,88,110,172,254,313,314,376,416,453,507,518,537/Binding site: carbohydrate

Query Match 10.0%; Score 162.5; DB 2; Length 557;

Best Local Similarity 22.0%; Pred. No. 9.2e-07;

Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;

QY 21 YALIPCLLTDEVALIPAPONLSVLTNNKRLHLMSPVIAPGETVYVSVEYQGEYESTLYT- 79

215 YSPVHCICKTIVENLEPPENIEVSQONQVYLK-----DYTYAMNTPQVOMLHAFK 267

QY 80 ----SHWITSSWCSLTGEGPCDVTDDITATVPYN-----LRVRLTGLSQTSAWS-- 125

268 RNPGRNHLX---KWKQI---PDCEVNTKTCQVFPQNPQKGIYILRVQASDQNTNFSWSEE 321

QY 126 -----ILKHPRNRNSTILTRPGMEIXKXGFHLVI-----ELELDLGPQREF 165





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Query Match      7.7%; Score 125.5; DB 2; Length 575;
Best Local Similarity 20.4%; Pred. No. 0.0021;
Matches 64; Conservative 53; Mismatches 121; Indels 75; Gaps 12;

OY 23 LIPCLLT-----DEVAL--LPAPQLSVLSTNMKHLMMSPVIAPEGTVYSVEVOGE 73
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 5 LLPPLVTISLSLEFIAYGTGLPSPSYVMPEARFQIILMKPIPNOSSEITVEALK-- 62
OY 74 YSLTSHWIFSSWSKSLDEGPCDVT---DDITATVPYNLRVRATLGQSOTSAMSLIKH 129
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 63 ---QGNSFWNDIHICRKAQALSCDLTFETFLDYHRSGYRARARADVNSQSWMTTET 119
OY 130 PENRNSTILT-----RGMEIXKKGFHLVIELELGPQFEELVAWMX 171
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 120 RTTYDEVILLTDSVTLKANDCGITYGIHPRPPIITPAAGDEDOVFCKL-RVYKTSIRKFS 178
OY 172 RRRGAEEHYKM-VRSGGIPVHLETMBEGAAYCYAKQTQFAIGXSAFSOTECYEVOGEA 230
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 179 ELKNATRKVKQETFTLVPIGR-----KFCVKVLPRLESRIKAMMSEGQCILLITEQ 232
OY 231 I-----PLVALAFVFGFMILLVVPLFVKMGRLLOYSCCPVVVL----- 271
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 233 YFTVTNLSTLVISMLEFCG-IIVCLVLQWIYIRHGKL-----PTVLVFKKHDFFPANP 285
OY 272 -----PDCLKTN 279
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 286 LCPETPDAIHVD 298

RESULT 12
A31555
Interferon gamma receptor precursor - human
C:Species: Homo sapiens (man)
C:Date: 28-Feb-1990 #sequence_revision 28-Feb-1990 #text_change 23-Jul-1999
C:Accession: A31555
R:Aguet, M.; Dembic, Z.; Meriin, G.
Cell 55, 273-280, 1988
A>Title: Molecular cloning and expression of the human interferon-gamma receptor
A:Reference number: A31555; MIDID:89003065
A:Molecule type: mRNA
A:Accession: A31555
A:Cross-references: GB:J03143; NID:g184650; PIDN:AAA52731.1; PID:g306915
C:Genetics:
A:Gene: GDB:IFNGRL; IFNGR
A:Cross-references: GDB:I20688; OMIM:107470
Map position: 6q23-q24
Superfamily: Interferon gamma receptor
Keywords: cytokine receptor; transmembrane protein

Query Match      7.4%; Score 121; DB 2; Length 489;
Best Local Similarity 21.6%; Pred. No. 0.0043;
Matches 61; Conservative 54; Mismatches 102; Indels 66; Gaps 13;

OY 35 LPAPQLSVLSTNMKHLMMSPVIAPEGTVY-----YSTEYOGEYSLTSHWIPSSW 88
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 29 VPTPPNVTTIESINMPVIYWEYOIMPQVPEFYEVKRYGK-----NSEKIDA-- 76
OY 89 CSLTGPECEDVTDITATVPYN--LRVRATLGQSOTSAMSLIKHFRNRNSTILTRPGMEI 145
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 77 CINIISHYCNIISDHVD--PSNSLMWRKVARKVQGESAVAKSEEFACRDKIGPKRKDI 134
OY 146 KXXGHVLVEL-----EDLGPFQF-FLVAY-WXRRPGADEHYKAWRSG--- 186
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 135 KRKEQIMIDITHPSVFNVGDEQVDYDPETTCYIRANYNYVRANGSEIOYKILTOEKED 194
OY 187 -----GIPVHLETMBEGAAYCYAKQTQFAIGXSAFSOTECYEVOGEA-----IP 232
   |||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||::|||
Db 195 GDEIQQLAIPIV-----SLNSQYCVSAGEVLHWGVYTEKSKEVCITIFNSSINGSLMIP 250
OY 233 LVIALFAFVFGFMILLVVPLFVKMGRLLOYSCCPVVVLDTLT 275

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Db      251 VVALLLFL--VLSLVFICFYIKRIINPLKEKS-----IILPSKL 287
                                                                    :|: :| | | : :| :| :| :| :|
RESULT  13
tissue factor precursor - mouse
KFMS3
N.Alternate names: coagulation factor III
C.Species: Mus musculus (house mouse)
C.Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 22-Jun-1999
C.Accession: A52318; A:39046
R.Hartzell, S.; Ryder, K.; Lanahan, A.; Lau, L.F.; Nathans, D.
MOL. Cell. Biol. 9, 2567-2573, 1989
A.Title: A growth factor-responsive gene of murine BALB/C 3T3 cells encodes a protein
A.Reference number: A52318; MUID:89343974
A.Accession: A52318
A.Molecule type: mRNA
A.Residues: 1-294 <HAB>
A.Cross-references: GB:M6071; NID:g201924; PIDN:AAA40414.1; PID:g201925
R.Ranganathan, G.; Blatt, S.P.; Subramaniam, M.; Pass, D.N.; Mathie, N.J.; Getz, M.J.
J. Biol. Chem. 266, 496-501, 1991
A.Title: Cloning of murine tissue factor and regulation of gene expression by transfo
A.Reference number: A59046; MUID:91093171
A.Accession: A59046
A.Molecule type: mRNA
A.Residues: 1-25, 'I', 27-294 <RAN>
A.Cross-references: GB:M57896; GB:J05713; NID:g201926; PIDN:AAA63400.1; PID:g201927
A.Note: 26-Thr was also found
C.Comment: Tissue factor is an integral membrane glycoprotein that serves as a recept
C.Comment: Expression of tissue factor can be induced in a variety of tissues by cert
C.Superfamily: tissue factor
C.Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembr
F:1-29/Domain: signal sequence #status predicted <SIG>
F:1-29/4/Product: tissue factor #status predicted <MAT>
F:30-251/Domain: extracellular #status predicted <EXT>
F:252-274/Domain: transmembrane #status predicted <TM>
F:37-57,169,200/Binding site: carbohydrate (asn) (covalent) #status predicted
F:75-83,218-241/Disulfide bonds: #status predicted
F:275/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match          7.2%; Score 116.5; DB 1; Length 294;
Best Local Similarity 23.3%; Pred. No. 0.006;
Matches 74; Conservative 38; Mismatches 116; Indels 89; Gaps 17;

QY  22 ALIP-----CLLDEVALIPAPQ--NLAVLSTNMKHLMLMSPVIAPGETVY-YSEYQGE 73
    ||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  12 ALAPFLICGLLQVYRAGAGIPKAFNLWISDFILEMQ-----PKPTNTTYTQISDR 67

QY  74 YESLYTSHTWIPSSMCSLGEPCVTDIT--ATVPYNLRVATL-----GSGQ--- 120
    ||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  68 -----SRNW--KNKCFSTDTEDCLTDEIVADVTWAEAKVLVSRPNRSVHGDDQLVI 119

QY  121 -----TSAMSLILKHPFRNRSTILLRPGME-----LKKXGFHLVI 154
    ||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  120 KEEPPFTNAPFLFP-----RDTNLGQPVYIQGFEDGKRKNLVVAKDSLTVRKKNSTFLTL 175

QY  155 ELEDLGPQEPFLVAV-WKREPGEAEHVKAVRSGGIPVHLETWEPGAAYC--VKAQTFVKA 211
    ||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  176 R-QVVGKDLGYIITIRKSGSTGKTKNITNTNFSIDV-----EEGVSCFVQAAMIFSRK 229

QY  212 IGXYSAFQSOTECV-----VQGEAIPLVIALFAVGFMLLVVVPFLVFKMKGRLLQYSCCP 267
    ||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  230 TQNSPGSGSVTCEQWKSFLGETLLIIGAVVLLATFIILLISLCKRRKRNRAGQ----- 284

QY  268 VVVLDPYTLKRTNSPKRL 284
    ||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db  285 -----GKKNTPSKRL 293
    ||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||

RESULT  14
KFBO3
tissue factor precursor - bovine

```

N:Alternate names: coagulation factor III  
 C:Species: Bos primigenius taurus (cattle)  
 C>Date: 30-Sep-1993 #sequence\_revision 30-Sep-1993 #text\_change 22-Jun-1999  
 C:Accession: J01319  
 R:Tokuyoshi, Y.; Muta, T.; Miyata, T.; Iwanaga, S.  
 Biochem. Biophys. Res. Commun. 181, 1145-1150, 1991  
 A:Title: cDNA and amino acid sequences of bovine tissue factor.  
 A:Reference number: J01319; MUID:92109720  
 A:Accession: J01319  
 A:Molecule type: mRNA  
 A:Residues: 1-292 <TAK>  
 A:Cross-references: GB:574147; NID:g241438; PIDN:AA20755.1; PID:g241439  
 A:Experimental source: adrenal gland  
 A:Note: part of this sequence, including the amino end of the mature protein, was confirmed by N-terminal sequencing.  
 C:Comment: Tissue factor is an integral membrane glycoprotein that serves as a receptor for Factor VII.  
 C:Superfamily: tissue factor  
 C:Keywords: blood coagulation; glycoprotein; lipoprotein; thiolester bond; transmembrane protein  
 F:1-35/Domain: signal sequence #status predicted <SIG>  
 F:36-292/Product: tissue factor #status experimental <EXT>  
 F:36-248/Domain: extracellular #status predicted <EXT>  
 F:249-271/Domain: transmembrane #status predicted <EXT>  
 F:272-292/Domain: intracellular #status predicted <INT>  
 F:43,153,181/Binding site: carbohydrate (Asn) (covalent) #status predicted  
 F:81-89,215-238/Disulfide bonds: #status predicted  
 F:118,124/Binding site: carbohydrate (Thr) (covalent) #status predicted  
 F:274/Binding site: palmitate (Cys) (covalent) #status experimental

Query Match 7.0%; Score 114.5; DB 1; Length 292;  
 Best Local Similarity 19.8%; Pred. No. 0.009;  
 Matches 49; Conservative 39; Mismatches 103; Indels 57; Gaps 9;

40 NLSTVSTMKHLLMSPYAPGEVYVSEYGESELTSTSHI-----MIPSSWCSLNE 93  
 DB 43 NITKSTFKTLEWEP-----KPINHYTVVISPRLGWN--KNKCFYTT 85  
 QY 94 GPECDVTDITATVYPLNLRVATLIGQTSAMSILKHPNRM-----STILLRPMGE-I 145  
 DB 86 NTECDVDEIVKVNREYTLARVLSYPADTSSSTVEPFPNPFYLETNLNGOPTIQSF 145  
 QY 146 KXGFEHLVLEED-----LGPFEFLVAYKXRGAEHVKMVASGCI 188  
 DB 146 EOVGTQKLVTVODARTLVANSAPFLSDRVFGKDLNLTLYKASSTGGKKATTNNNG-- 203  
 QY 189 PVHETMPGACVCAKQDFV--KAIGXYSAFSQTECEVGEAIPLVLAFAVGFMLI 246  
 DB 204 --FLIDVKGKGYCHVOAVIISRVNOKSPSPITKTSHEK---VLSTELFFIIGTVM 258  
 QY 247 LVVYPLFV 254  
 DB 259 VIIIFIV 266

RESULT 15  
 A32385  
 erythropoietin receptor precursor, membrane-bound form - mouse  
 C:Species: Mus musculus (house mouse)  
 C>Date: 28-Sep-1990 #sequence\_revision 05-Apr-1995 #text\_change 22-Jun-1999  
 C:Accession: A41686; A32385; S13249  
 R:Hino, M.; Tojo, A.; Misawa, Y.; Morii, H.; Takaku, F.; Shibuya, M.  
 Mol. Cell. Biol. 11, 5527-5533, 1991  
 A:Title: Unregulated expression of the erythropoietin receptor gene caused by insertion  
 A:Reference number: A41686; MUID:92017832  
 A:Accession: A41686  
 A:Molecule type: mRNA  
 A:Residues: 1-507 <HIN>  
 A:Cross-references: GB:S59388; NID:g237036; PIDN:AA20029.1; PID:g237037  
 A:Experimental source: murine erythrocytopenia (MEU) cell line F5-3  
 R:D'Andrea, A.D.; Lodish, H.F.; Wong, G.G.  
 Cell 57, 277-285, 1989  
 A:Title: Expression cloning of the murine erythropoietin receptor.  
 A:Reference number: A32385; MUID:89195238

A:Accession: A32385  
 A:Molecule type: mRNA  
 A:Residues: 1-507 <DAA>  
 A:Cross-references: GB:004843; NID:g193090; PIDN:AA37571.1; PID:g309219  
 A:Experimental source: murine erythrocytopenia (MEU) cells, subclone 745  
 R:Kuramochi, S.; Ikawa, Y.; Todokoro, K.  
 J. Mol. Biol. 216, 567-575, 1990  
 A:Title: Characterization of murine erythropoietin receptor genes.  
 A:Reference number: S13249; MUID:91080149  
 A:Accession: S13249  
 A:Molecule type: DNA; mRNA  
 A:Residues: 1-507 <KOR>  
 A:Cross-references: EMBL:X53081; NID:g50861; PIDN:CAA37248.1; PID:g50862  
 A:Experimental source: murine erythrocytopenia K-1 cells  
 C:Genetics:  
 A:Introns: 39/1; 83/2; 142/1; 194/3; 246/1; 275/2; 304/3  
 C:Superfamily: erythropoietin receptor; cytokine receptor homology  
 C:Keywords: alternative splicing; cytokine receptor; glycoprotein; transmembrane protein  
 F:1-24/Domain: signal sequence #status predicted <SIG>  
 F:25-507/Product: erythropoietin receptor #status predicted <EXT>  
 F:25-249/Domain: extracellular #status predicted <EXT>  
 F:52-238/Domain: cytokine receptor homology <CRS>  
 F:250-271/Domain: transmembrane #status predicted <TMN>  
 F:272-507/Domain: intracellular #status predicted <INT>  
 F:52-62,90-106/Disulfide bonds: #status predicted  
 F:75/Binding site: carbohydrate (Asn) (covalent) #status predicted

Query Match 7.0%; Score 114; DB 1; Length 507;  
 Best Local Similarity 23.2%; Pred. No. 0.019;  
 Matches 73; Conservative 39; Mismatches 98; Indels 104; Gaps 18;

QY 26 CLLTDEVAIPAP-----QNLSTVSTMKHLL-MSPVIAPEVTV 65  
 DB 16 CLLAGAAAPSPSLPPEKESKALLASGSEELCTQKLELVCEWMAASGDFN 75  
 QY 66 YSEYGESESLYTHIMIPSSWCSLNEGPE-----CDV-TDITATVYPLNLRVAT 116  
 DB 76 YSEYGESESLYTHIMIPSSWCSLNEGPE-----CDV-TDITATVYPLNLRVAT 116  
 QY 117 LGS-----QTSAMSLIKHPFNNSITLIRPGMEIKKXGHLVLEEDLGPFEFLVAY 169  
 DB 127 SGSPRRHRIIHNELVLDAP-----AGILARRAE--GSHVLR----- 164  
 QY 170 WKEPFGA--EENYKVN-----RSGGIPVLEFMEPGACVCAQO-----TF-YKA- 211  
 DB 165 WLPFGAPMTTHIRYEDVSNAGNAGSTQ-RVEVLE-GRTCVLSNLRGRTYFAVARAR 222  
 QY 212 -----IGXYSASFQTECEVGEAIPLVLAFAVGFMLLVVYPLFVWKMKG-----RL 260  
 DB 223 MAEPFSFGFMSAMSEPAISLTASDLDPLILTL-----SLIVLISLLFVLAALLSHRRT 276  
 QY 261 LQYSCCPVVVLPPT 274  
 DB 277 LQCKIMPPIPSPES 290

Search completed: October 12, 2001, 16:10:38  
 Job time: 115 sec





GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 12, 2001, 16:08:23 ; Search time 12.3 Seconds  
(without alignments)  
520.618 Million cell updates/sec

Title: US-09-265-540E-2

Perfect score: 1627  
Sequence: 1 MDTFTVLEIWTSLFMWFF.....VDACAVVMSPEELRAWIS 311

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 197339 seqs, 20590346 residues

Fail number of hits satisfying chosen parameters: 197339

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

Issued\_Patents\_AA.\*  
1: /cgn2\_6/ptodata/2/1aa/5A.COMB.pep.\*  
2: /cgn2\_6/ptodata/2/1aa/5B.COMB.pep.\*  
3: /cgn2\_6/ptodata/2/1aa/6A.COMB.pep.\*  
4: /cgn2\_6/ptodata/2/1aa/6B.COMB.pep.\*  
5: /cgn2\_6/ptodata/2/1aa/PCVUS.COMB.pep.\*  
6: /cgn2\_6/ptodata/2/1aa/backfiles1.pep.\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Match | Length | DB ID | Description      |
|------------|-------|-------|--------|-------|------------------|
| 1          | 191   | 11.7  | 325    | 2     | US-08-683-743-4  |
| 2          | 176.5 | 10.8  | 337    | 5     | PCT-US94-14277-8 |
| 3          | 162.5 | 10.0  | 557    | 1     | US-08-328-256-10 |
| 4          | 162.5 | 10.0  | 557    | 1     | US-08-471-454-2  |
| 5          | 162.5 | 10.0  | 557    | 2     | US-08-466-974-2  |
| 6          | 162.5 | 10.0  | 557    | 2     | US-08-471-453-2  |
| 7          | 162.5 | 10.0  | 557    | 2     | US-08-307-588-4  |
| 8          | 157   | 9.6   | 332    | 5     | PCT-US94-14277-2 |
| 9          | 146   | 9.0   | 223    | 5     | PCT-US94-14277-6 |
| 10         | 138   | 8.5   | 553    | 2     | US-08-943-087-14 |
| 11         | 138   | 8.5   | 553    | 2     | US-08-943-087-16 |
| 12         | 138   | 8.5   | 553    | 2     | US-08-943-087-18 |
| 13         | 138   | 8.5   | 553    | 2     | US-08-943-087-20 |
| 14         | 138   | 8.5   | 553    | 2     | US-08-943-087-22 |
| 15         | 138   | 8.5   | 553    | 2     | US-08-943-087-24 |
| 16         | 138   | 8.5   | 553    | 2     | US-08-943-087-26 |
| 17         | 138   | 8.5   | 553    | 2     | US-08-943-087-28 |
| 18         | 138   | 8.5   | 553    | 2     | US-08-943-087-30 |
| 19         | 138   | 8.5   | 553    | 2     | US-08-943-087-32 |
| 20         | 138   | 8.5   | 553    | 2     | US-08-943-087-34 |
| 21         | 138   | 8.5   | 553    | 2     | US-08-943-087-36 |
| 22         | 138   | 8.5   | 553    | 2     | US-08-943-087-38 |
| 23         | 138   | 8.5   | 553    | 2     | US-08-943-087-40 |
| 24         | 138   | 8.5   | 553    | 2     | US-08-943-087-42 |
| 25         | 138   | 8.5   | 553    | 2     | US-08-943-087-44 |
| 26         | 138   | 8.5   | 553    | 2     | US-08-943-087-46 |
| 27         | 138   | 8.5   | 553    | 2     | US-08-943-087-48 |

|    |       |     |     |   |                  |                   |
|----|-------|-----|-----|---|------------------|-------------------|
| 28 | 138   | 8.5 | 553 | 2 | US-08-943-087-48 | Sequence 48, Appl |
| 29 | 137.5 | 8.5 | 221 | 2 | US-08-943-087-54 | Sequence 54, Appl |
| 30 | 137.5 | 8.5 | 434 | 1 | US-08-328-256-11 | Sequence 11, Appl |
| 31 | 136.5 | 8.4 | 436 | 2 | US-08-307-588-5  | Sequence 2, Appl  |
| 32 | 136   | 8.4 | 578 | 1 | US-08-424-788-5  | Sequence 5, Appl  |
| 33 | 136   | 8.4 | 578 | 1 | US-08-110-683-2  | Sequence 2, Appl  |
| 34 | 136   | 8.4 | 578 | 2 | US-08-683-743-2  | Sequence 2, Appl  |
| 35 | 136   | 8.4 | 578 | 2 | US-08-477-166-2  | Sequence 2, Appl  |
| 36 | 136   | 8.4 | 578 | 2 | US-08-472-097-2  | Sequence 2, Appl  |
| 37 | 136   | 8.4 | 578 | 5 | PCT-US93-11638-2 | Sequence 2, Appl  |
| 38 | 135.5 | 8.3 | 221 | 2 | US-08-943-087-52 | Sequence 52, Appl |
| 39 | 135.5 | 8.3 | 221 | 2 | US-08-943-087-58 | Sequence 58, Appl |
| 40 | 134.5 | 8.3 | 221 | 2 | US-08-943-087-56 | Sequence 56, Appl |
| 41 | 133.5 | 8.2 | 221 | 2 | US-08-943-087-50 | Sequence 50, Appl |
| 42 | 131.5 | 8.1 | 221 | 2 | US-08-943-087-60 | Sequence 60, Appl |
| 43 | 131   | 8.1 | 200 | 5 | PCT-US94-14277-4 | Sequence 4, Appl  |
| 44 | 128.5 | 7.9 | 557 | 1 | US-08-424-788-6  | Sequence 6, Appl  |
| 45 | 126.5 | 7.8 | 408 | 2 | US-08-683-007A-2 | Sequence 2, Appl  |

#### ALIGNMENTS

RESULT 1  
US-08-683-743-4  
; Sequence 4, Application US/08683743  
; Patent No. 5843697  
; GENERAL INFORMATION:  
; APPLICANT: Pestka, Sidney  
; APPLICANT: Kotenko, Sergey  
; TITLE OF INVENTION: CYTOKINE RECEPTOR SIGNAL TRANSDUCTION  
; TITLE OF INVENTION: CHAIN  
; NUMBER OF SEQUENCES: 25  
; CORRESPONDENCE ADDRESS:  
; ADDRESSEE: David A. Jackson, Esq.  
; STREET: 411 Hackensack Ave, Continental Plaza, 4th  
; STREET: Floor  
; CITY: Hackensack  
; STATE: New Jersey  
; COUNTRY: USA  
; ZIP: 07601  
; COMPUTER READABLE FORM:  
; MEDIUM TYPE: Floppy disk  
; COMPUTER: IBM PC compatible  
; OPERATING SYSTEM: PC-DOS/MS-DOS  
; SOFTWARE: Patent Release #1.0, Version #1.30  
; CURRENT APPLICATION DATA:  
; APPLICATION NUMBER: US/08/683,743  
; FILING DATE: 17-JUL-1996  
; CLASSIFICATION: 435  
; ATTORNEY/AGENT INFORMATION:  
; NAME: Jackson Esq., David A.  
; REGISTRATION NUMBER: 26,742  
; REFERENCE/DOCKET NUMBER: 601-1-050  
; TELECOMMUNICATION INFORMATION:  
; TELEPHONE: 201-487-5800  
; TELEFAX: 201-343-1684  
; INFORMATION FOR SEQ. ID NO. 4:  
; SEQUENCE CHARACTERISTICS:  
; LENGTH: 325 amino acids  
; TYPE: amino acid  
; STRANDEDNESS: single  
; TOPOLOGY: linear  
; MOLECULE TYPE: protein  
; HYPOTHETICAL: NO  
; FRAGMENT TYPE:  
; ;  
; US-08-683-743-4

Query Match 11.7%; Score 191; DB 2; Length 325;  
Best Local Similarity 26.6%; Pred. No. 1,4e-12;  
Matches 77; Conservative 47; Mismatches 117; Indels 48; Gaps 16;

QY 12 WTSLEFMWFEVALIPCLLIDVAILAPONLSVLTNNKHLMM--SPVIAEGEYVYSEY 70  
 Db 3 W-SLGS- ---LGGLYSALGAVPPENVMNSVNFKNILQWESPFAK- ---NLTJE 52  
 QY 71 QGESESYTSHIWIPISSWCSLTGEGPCDVTDDITATVPYNLRVATGSGQTSAM-SILKH 129  
 Db 53 TAQYLSTR-----IFOKKANTITTECDFS-SLSKYGDHILRVARAFRDESDMVAITFC 106  
 QY 130 PFNRNSTILTRPGMEIKXGFHLYIELEDLQPOE-----FLVAYXRE 173  
 Db 107 PV--DDITIPPGQVLEVLADSL--HMRFLAPKLENEFETWTKMNYNSWTYNYQW--K 160  
 QY 174 PGAEHYKAVRSGCIPVHLEMERGAAYCYKAQTFVKAIGYSAFSQTEVE-VQGEAIP 232  
 Db 161 NGDEKFOIRPOYDFEV-LRNLBFWTYCYQVRGFLPDRNKGEMSEPCQTHDETVP 219  
 QY 233 ---LVIALFAVFGFMLLVVPLF--VWKMGRLQYSGCCPVVLPDILK 276  
 220 SMVAVILMASV-FWCLALLGCFSLIMCYKTKTVAFSPRNSLPOHLK 267

RESULT 2  
 PCT-US94-14277-8  
 ; Sequence 8, Application PC/TUS9414277  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Aguet, Michel  
 ; APPLICANT: Bohni, Ruth  
 ; APPLICANT: Hemmi, Silvio  
 ; TITLE OF INVENTION: Receptor Subunit Polypeptides  
 ; NUMBER OF SEQUENCES: 8  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: Genentech, Inc.  
 ; STREET: 460 Point San Bruno Blvd  
 ; CITY: South San Francisco  
 ; STATE: California  
 ; COUNTRY: USA  
 ; ZIP: 94080  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: patin (Genentech)  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: PCT/US94/14277  
 ; FILING DATE: 07-DEC-1994  
 ; CLASSIFICATION:  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: 08/164596  
 ; FILING DATE: 09-DEC-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: Love, Richard B.  
 ; REGISTRATION NUMBER: 34,659  
 ; REFERENCE/DOCKET NUMBER: 866PCT  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 415/225-5530  
 ; TELEFAX: 415/952-9881  
 ; TELEX: 910/371-7168  
 ; INFORMATION FOR SEQ ID NO: 8:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 337 amino acids  
 ; TYPE: amino acid  
 ; TOPOLOGY: linear  
 ; PCT-US94-14277-8

Query Match 10.88; Score 176.5; DB 5; Length 337;  
 Best Local Similarity 25.88; Pred. No. 5.5e-11;  
 Matches 74; Conservative 43; Mismatches 123; Indels 47; Gaps 14;

QY 11 WTSLEFMWFEVALIPCLLIDVAILAPONLSVLTNNKHLMMSPVIAEGEYVYSEY 68  
 Db 6 LMSLLILGFAFAAAAPRPPISQLPAPQHPKIRLYNAEQVLSWEPVALSNSTRFVYQV 65

QY 69 EYQGESESYTSHIWIPISSWCSLTGEGPCDVTDDITATVP-----YNLRVATIGS 119  
 Db 66 QEKYDSKMFADIASIGVNCITATATEC-----DEFAASPSAGFPMDFNVTLRRAELGA 121  
 QY 120 QTSAMSL---KHPNRNSTILTRPGMEIKXGFHLYI-----ELEDLQPOE-FLVAY 169  
 Db 122 LHSAAVWMPFQH--YRNVATGPPENIEVTPGEGSLITRFSSPFIDATSTAFPCYVAY 179  
 QY 170 WAREPGEAEHYK-MYRSGCIPVHLEMERGAAYCYKAQ-----TFVKAIGYSAFSQ 221  
 Db 180 W-EMGQIQYKGRPRNSI--SLDNKPRRYCCIQVQAQALLMNSNIFRVCHLSNIS-- 233  
 QY 222 ECVEYQGEA-IPVIALFAVFGFMLLVVPLF--LVWKMGRLQY 263  
 Db 224 -CYDTMADASTELQOVILISVCTFSLSYLAGACFVLKYGRLKY 279

RESULT 3  
 US-08-328-256-10  
 ; Sequence 10, Application US/08328256  
 ; Patent No. 5643749  
 ; GENERAL INFORMATION:  
 ; APPLICANT: Revel, Michel  
 ; APPLICANT: ABRAMOVICH, Carolina  
 ; APPLICANT: RATOVIJSKI, Edward  
 ; TITLE OF INVENTION: SOLUBLE INTERFERON ALPHA-RECEPTOR, ITS  
 ; PREPARATION AND USE  
 ; NUMBER OF SEQUENCES: 12  
 ; CORRESPONDENCE ADDRESS:  
 ; ADDRESSEE: BROWDY AND NEIMARK  
 ; STREET: 419 Seventh Street, N.W., Suite 300  
 ; CITY: Washington  
 ; STATE: D.C.  
 ; COUNTRY: USA  
 ; ZIP: 20004  
 ; COMPUTER READABLE FORM:  
 ; MEDIUM TYPE: Floppy disk  
 ; COMPUTER: IBM PC compatible  
 ; OPERATING SYSTEM: PC-DOS/MS-DOS  
 ; SOFTWARE: Patentin Release #1.0, Version #1.30  
 ; CURRENT APPLICATION DATA:  
 ; APPLICATION NUMBER: US/08/328,256  
 ; FILING DATE: 24-OCT-1994  
 ; PRIOR APPLICATION DATA:  
 ; APPLICATION NUMBER: IL 107378  
 ; FILING DATE: 24-OCT-1993  
 ; ATTORNEY/AGENT INFORMATION:  
 ; NAME: BROWDY, Roger L.  
 ; REGISTRATION NUMBER: REVEL-13  
 ; REFERENCE/DOCKET NUMBER: 25,618  
 ; TELECOMMUNICATION INFORMATION:  
 ; TELEPHONE: 202-628-5197  
 ; TELEFAX: 202-737-3528  
 ; TELEX: 248633  
 ; INFORMATION FOR SEQ ID NO: 10:  
 ; SEQUENCE CHARACTERISTICS:  
 ; LENGTH: 557 amino acids  
 ; TYPE: amino acid  
 ; STRANDEDNESS: single  
 ; TOPOLOGY: linear  
 ; MOLECULE TYPE: protein  
 ; US-08-328-256-10

Query Match 10.08; Score 162.5; DB 1; Length 557;  
 Best Local Similarity 22.08; Pred. No. 3.7e-09;  
 Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;

QY 21 VALIPCLLIDVAILAPONLSVLTNNKHLMMSPVIAEGEYVYSEYQGESESYT- 79  
 Db 215 YSPVACIKRTYVENLRPPENIEVSQVONQYVLK-----DYTYANMTPQVQMLAFLAK 267  
 QY 80 ---SHIWIPISSWCSLTGEGPCDVTDDITATVPYN-----LRVRATIGSQTSAWS-- 125

Db 268 RNPGRNHLTY---KWKQI---PDCENVKTTQCVFPQNVFOKGITLLKVAQASDGNNTSFWSEB 321  
QY 126 -----ILKHPNRNSTILTRPGMEIKKGFHLVY-----ELEDLGPQFER 165  
Db 322 IKFDEIQAFLPLPPVFNIRS-----LSDSFHIYIGAPKOSGNTPVYIDYPLIYE- 370  
QY 166 LVAYWAKREPGEAEHVWVSGGIPVHLETPMEPGAAYCVKAO--TFVKAIGXSAFSQTEC 223  
Db 371 -IIFWENTSNAERKITEKT---DVTVPNLKPLTVYCVKRAHNTDEKLNKSSVFSDAVC 426  
QY 224 VEOV-GEAIPVLYALFAPVGMILLVVPVLFVWKMGRLLQYSCCPVVPVLPDTLKTINS-- 280  
Db 427 EKTKEPNTSKIML---IVGICIALFALPLPVYIAKVFRL--CINVYFEP-SLKPSSSID 479  
QY 281 -----PQK--LISCREEVDAC 295  
Db 480 EYFSEQPLKNLLSTSEQIEKC 502

RESULT 4  
US-08-471-454-2  
Sequence 2, Application US/08471454  
Patent No. 5731169  
GENERAL INFORMATION:  
APPLICANT: MOGENSEN, Knud E.  
APPLICANT: UZE, Gilles  
APPLICANT: LUTFALLA, Georges  
APPLICANT: GRESSER, Ion  
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR  
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHUYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/471,454  
CLASSIFICATION: 435  
FILING DATE: 06-JUN-1995  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/900,642  
FILING DATE: 15-JUN-1992  
APPLICATION NUMBER: FR 89/13770  
FILING DATE: 20-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 960-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
US-08-471-454-2

Query Match 10.0%; Score 162.5; DB 1; Length 557;

Best Local Similarity 22.0%; Pred. No. 3.7e-09;  
Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;  
QY 21 VALIPCLLDEVAAILAPONLSVLSSTNMKLLMMSPIVIAAGEVYVSVGEYESTLYT- 79  
Db 215 YSPVHCITKTVNELPPEPIEVSQNONVYLMK-----DITYANMTQVOMLHAFK 267  
QY 80 ----SHIWISSWCSLTGEPEDVTDITATVYN-----LRYRATIGSOTSAMS- 125  
Db 268 RNPGRNHLTY---KWKQI---PDCENVKTTQCVFPQNVFOKGITLLKVAQASDGNNTSFWSEB 321  
QY 126 -----ILKHPNRNSTILTRPGMEIKKGFHLVY-----ELEDLGPQFER 165  
Db 322 IKFDEIQAFLPLPPVFNIRS-----LSDSFHIYIGAPKOSGNTPVYIDYPLIYE- 370  
QY 166 LVAYWAKREPGEAEHVWVSGGIPVHLETPMEPGAAYCVKAO--TFVKAIGXSAFSQTEC 223  
Db 371 -IIFWENTSNAERKITEKT---DVTVPNLKPLTVYCVKRAHNTDEKLNKSSVFSDAVC 426  
QY 224 VEOV-GEAIPVLYALFAPVGMILLVVPVLFVWKMGRLLQYSCCPVVPVLPDTLKTINS-- 280  
Db 427 EKTKEPNTSKIML---IVGICIALFALPLPVYIAKVFRL--CINVYFEP-SLKPSSSID 479  
QY 281 -----PQK--LISCREEVDAC 295  
Db 480 EYFSEQPLKNLLSTSEQIEKC 502

RESULT 5  
US-08-466-974-2  
Sequence 2, Application US/08466974  
Patent No. 5861258  
GENERAL INFORMATION:  
APPLICANT: MOGENSEN, Knud E.  
APPLICANT: UZE, Gilles  
APPLICANT: LUTFALLA, Georges  
APPLICANT: GRESSER, Ion  
TITLE OF INVENTION: CDNA FRAGMENT CODING FOR THE GENE FOR  
TITLE OF INVENTION: THE ALPHA INTERFERON RECEPTOR AND PROCESS FOR THE  
NUMBER OF SEQUENCES: 2  
CORRESPONDENCE ADDRESSES:  
ADDRESSEE: NIXON & VANDERHUYE P.C.  
STREET: 1100 NORTH GLEBE ROAD  
CITY: ARLINGTON  
STATE: VIRGINIA  
COUNTRY: U.S.A.  
ZIP: 22201-4714  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/466,974  
FILING DATE: 06-JUN-1995  
CLASSIFICATION: 435  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: US 07/900,642  
FILING DATE: 15-JUN-1992  
APPLICATION NUMBER: FR 89/13770  
FILING DATE: 20-OCT-1989  
ATTORNEY/AGENT INFORMATION:  
NAME: BYRNE, THOMAS E.  
REGISTRATION NUMBER: 32,205  
REFERENCE/DOCKET NUMBER: 960-7  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: (703) 816-4000  
TELEFAX: (703) 816-4100  
TELEX: 200797 NIXN UR  
INFORMATION FOR SEQ ID NO: 2:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 557 amino acids









APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 18:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-943-087-18

Query Match 8.5%; Score 138; DB 2; Length 553;  
Best Local Similarity 21.3%; Pred. No. 1.7e-06;  
Matches 55; Conservative 43; Mismatches 98; Indels 62; Gaps 11;

QY 24 IPCLLDEVALIPAPONLSVLSTNMKHLMMSPVIA-PGETVYYSVYQGEYESLYTSHI 82  
DB 30 VPCVSGSGLPKRPAITFLSLNMKNVLOMTPEGLQGVKVTYVOY----FTYQKK 80  
QY 83 WIPSSWCSLTEGPCDVTDDIT-ATVPYNLRVATLGSQTSAM--SILKHPNNR----- 134  
DB 81 WLKSECRNINRYCDLSAETSDYEHQYAKVKAIMGTKSKMAESGRFYPLETQIGPP 140  
QY 135 -----STILTRPGMEIKKGFHLVIELEDLGPQEFVLAV-----WKREPG 175  
DB 141 EVALTTDEKSIYVLTAPEKMRNPEDLPVSMQOISNLTKNVSVLTKSNRTWSQ--C 197  
QY 176 AEHVKNVRSRGIPVHETMEPGAAYCYKQTFVKAIGXYSFQSOTCEVEQGE----- 229  
DB 198 VTNHTLV-----LWLEPNTLYCVHVESFVGPPTRRAPQSEKOCARTLKQSSSEFK 248  
QY 230 -----AIPVLALFAF 240  
DB 249 AKIIFWVLPISITVFLF 266

RESULT 14  
US-08-943-087-20  
Sequence 20, Application US/08943087  
Patent No. 5945511  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmeberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Farrah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Diskette  
COMPUTER: IBM Compatible

OPERATING SYSTEM: DOS  
SOFTWARE: FASTSEQ for Windows Version 2.0  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/943,087  
FILING DATE:  
CLASSIFICATION: 536  
PRIOR APPLICATION DATA:  
APPLICATION NUMBER: 08/803,305  
FILING DATE: 20-FEB-1997  
ATTORNEY/AGENT INFORMATION:  
NAME: Lunn, Paul G  
REGISTRATION NUMBER: 32,743  
REFERENCE/DOCKET NUMBER: 96-24C1  
TELECOMMUNICATION INFORMATION:  
TELEPHONE: 206-442-6627  
TELEFAX: 206-442-6678  
TELEX:  
INFORMATION FOR SEQ ID NO: 20:  
SEQUENCE CHARACTERISTICS:  
LENGTH: 553 amino acids  
TYPE: amino acid  
STRANDEDNESS: single  
TOPOLOGY: linear  
MOLECULE TYPE: protein  
FRAGMENT TYPE: internal  
US-08-943-087-20

Query Match 8.5%; Score 138; DB 2; Length 553;  
Best Local Similarity 21.3%; Pred. No. 1.7e-06;  
Matches 55; Conservative 43; Mismatches 98; Indels 62; Gaps 11;

QY 24 IPCLLDEVALIPAPONLSVLSTNMKHLMMSPVIA-PGETVYYSVYQGEYESLYTSHI 82  
DB 30 VPCVSGSGLPKRPAITFLSLNMKNVLOMTPEGLQGVKVTYVOY----FTYQKK 80  
QY 83 WIPSSWCSLTEGPCDVTDDIT-ATVPYNLRVATLGSQTSAM--SILKHPNNR----- 134  
DB 81 WLKSECRNINRYCDLSAETSDYEHQYAKVKAIMGTKSKMAESGRFYPLETQIGPP 140  
QY 135 -----STILTRPGMEIKKGFHLVIELEDLGPQEFVLAV-----WKREPG 175  
DB 141 EVALTTDEKSIYVLTAPEKMRNPEDLPVSMQOISNLTKNVSVLTKSNRTWSQ--C 197  
QY 176 AEHVKNVRSRGIPVHETMEPGAAYCYKQTFVKAIGXYSFQSOTCEVEQGE----- 229  
DB 198 VTNHTLV-----LWLEPNTLYCVHVESFVGPPTRRAPQSEKOCARTLKQSSSEFK 248  
QY 230 -----AIPVLALFAF 240  
DB 249 AKIIFWVLPISITVFLF 266

RESULT 15  
US-08-943-087-22  
Sequence 22, Application US/08943087  
Patent No. 5945511  
GENERAL INFORMATION:  
APPLICANT: Lok, Si  
APPLICANT: Kho, Choon J.  
APPLICANT: Jelmeberg, Anna C.  
APPLICANT: Adams, Robyn L.  
APPLICANT: Whitmore, Theodore E.  
APPLICANT: Farrah, Theresa M.  
TITLE OF INVENTION: CYTOKINE RECEPTOR  
NUMBER OF SEQUENCES: 60  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: ZymoGenetics, Inc.  
STREET: 1201 Eastlake Avenue East  
CITY: Seattle  
STATE: WA  
COUNTRY: USA  
ZIP: 98102





GenCore version 4.5  
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OK protein - protein search, using sw model

Run on: October 12, 2001, 16:06:48 ; Search time 20.8 Seconds  
(without alignments)  
906.445 Million cell updates/sec

Title: US-09-265-540E-2  
Perfect score: 1627  
Sequence: 1 MORTMYLEIETWTSLEFMWF.....VDACATVMSPEELLRAWIS 311

Scoring table:  
BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 412676 seqs, 60623988 residues  
Total number of hits satisfying chosen parameters: 412676

Minimum DB seq length: 0  
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

#### Database :

1: A.Geneseq\_0601.\*  
2: /SID8/gcgdata/geneseq/geneseq/AA1980.DAT.\*  
3: /SID8/gcgdata/geneseq/geneseq/AA1981.DAT.\*  
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16: /SID8/gcgdata/geneseq/geneseq/AA1994.DAT.\*  
17: /SID8/gcgdata/geneseq/geneseq/AA1995.DAT.\*  
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19: /SID8/gcgdata/geneseq/geneseq/AA1997.DAT.\*  
20: /SID8/gcgdata/geneseq/geneseq/AA1998.DAT.\*  
21: /SID8/gcgdata/geneseq/geneseq/AA2000.DAT.\*  
22: /SID8/gcgdata/geneseq/geneseq/AA2001.DAT.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description            |
|------------|-------|-------------|--------|-------|------------------------|
| 1          | 1620  | 99.6        | 311    | 20    | AAV41736 - <i>act</i>  |
| 2          | 1620  | 99.6        | 311    | 21    | AAAB44292 - <i>act</i> |
| 3          | 1620  | 99.6        | 311    | 21    | AAAB33440 - <i>act</i> |
| 4          | 1620  | 99.6        | 311    | 21    | AAAY97046 - <i>act</i> |
| 5          | 1620  | 99.6        | 311    | 21    | AAV44664 - <i>act</i>  |
| 6          | 1620  | 99.6        | 311    | 21    | AAV66676 - <i>act</i>  |
| 7          | 1620  | 99.6        | 311    | 22    | AAAB65199 - <i>act</i> |
| 8          | 1619  | 99.5        | 311    | 22    | AAV39472 - <i>act</i>  |
| 9          | 1243  | 76.4        | 308    | 21    | AAAY97048 - <i>act</i> |
| 10         | 529   | 32.5        | 100    | 21    | AAAG03609 - <i>act</i> |
| 11         | 191   | 11.7        | 325    | 19    | AAW52296 - <i>act</i>  |

|    |       |      |     |    |           |                    |
|----|-------|------|-----|----|-----------|--------------------|
| 12 | 191   | 11.7 | 325 | 22 | AAAB31214 | Amino acid sequenc |
| 13 | 179.5 | 11.0 | 337 | 16 | AAAB71035 | Human IFN-gamma ac |
| 14 | 176.5 | 10.8 | 337 | 13 | AAAB75783 | IFN-gamma receptor |
| 15 | 163.5 | 10.0 | 557 | 13 | AAAB28496 | Sequence of a soul |
| 16 | 162.5 | 10.0 | 557 | 12 | AAAB1958  | Human alpha-interf |
| 17 | 162.5 | 10.0 | 557 | 12 | AAAB14488 | Complete Interfero |
| 18 | 162.5 | 10.0 | 557 | 14 | AAAB2635  | Human Interferon r |
| 19 | 162.5 | 10.0 | 557 | 16 | AAAB21804 | Transmembranl int  |
| 20 | 162.5 | 10.0 | 557 | 21 | AAAB57094 | Human prostate can |
| 21 | 161.5 | 9.9  | 557 | 16 | AAAB75356 | Human IFN receptor |
| 22 | 157   | 9.6  | 332 | 16 | AAAB75782 | IFN-gamma receptor |
| 23 | 138   | 8.5  | 533 | 19 | AAAB79159 | Zeylor7 cytokine r |
| 24 | 137.5 | 8.5  | 434 | 16 | AAAB21805 | Spliced-deleted in |
| 25 | 136.5 | 8.4  | 436 | 12 | AAAB14487 | Soluble interferon |
| 26 | 136.5 | 8.4  | 436 | 13 | AAAB28495 | Sequence of a soul |
| 27 | 136   | 8.4  | 578 | 15 | AAAB57138 | Interleukin-10 rec |
| 28 | 136   | 8.4  | 578 | 19 | AAAB1804  | Human IL-10 recept |
| 29 | 133.5 | 8.2  | 436 | 16 | AAAB71723 | IFN receptor extra |
| 30 | 132   | 8.1  | 263 | 18 | AAAB17725 | Human tissue facto |
| 31 | 129   | 7.9  | 263 | 18 | AAAB17742 | Human tissue facto |
| 32 | 129   | 7.9  | 263 | 18 | AAAB17743 | Human tissue facto |
| 33 | 128   | 7.9  | 263 | 18 | AAAB17723 | Human tissue facto |
| 34 | 128   | 7.9  | 263 | 18 | AAAB17724 | Human tissue facto |
| 35 | 126.5 | 7.8  | 235 | 18 | AAAB1867  | Human tissue facto |
| 36 | 126.5 | 7.8  | 235 | 19 | AAAB48270 | Mature human tissu |
| 37 | 126.5 | 7.8  | 408 | 20 | AAAB4315  | Trx-rabbit tissue  |
| 38 | 126   | 7.7  | 263 | 18 | AAAB17744 | Human tissue facto |
| 39 | 126   | 7.7  | 263 | 18 | AAAB17745 | Human tissue facto |
| 40 | 126   | 7.7  | 263 | 18 | AAAB17719 | Human tissue facto |
| 41 | 125.5 | 7.7  | 295 | 9  | AAAB1503  | Human tissue facto |
| 42 | 125.5 | 7.7  | 295 | 9  | AAAB80504 | Sequence encoded b |
| 43 | 125.5 | 7.7  | 295 | 9  | AAAB80713 | Complete sequence  |
| 44 | 125.5 | 7.7  | 295 | 15 | AAAB5178  | Pre-hurFh Homo s   |
| 45 | 125.5 | 7.7  | 295 | 18 | AAAB31532 | Human tissue facto |

#### ALIGNMENTS

|          |  |                            |
|----------|--|----------------------------|
| RESULT 1 | AAV41736   | standard; Protein; 311 AA. |
| ID       | AAV41736   |                            |
| XX       |  |                            |
| AC       | AAV41736;  |                            |
| XX       |  |                            |
| DT       | 07-DEC-1999  | (first entry)              |
| XX       |  |                            |
| DE       | Human PRO1114  | protein sequence.          |
| XX       |  |                            |
| KW       | Human; PRO; EST; expressed sequence tag; PCR primer; hybridisation;    |                            |
| KW       | probe; blood coagulation disorder; cancer; cellular adhesion disorder; |                            |
| KW       | secreted protein; transmembrane protein.                               |                            |
| XX       |  |                            |
| OS       | Homo sapiens.  |                            |
| XX       |  |                            |
| PN       | W09946281-A2.  |                            |
| XX       |  |                            |
| PD       | 16-SEP-1999.   |                            |
| XX       |  |                            |
| PF       | 08-MAR-1999;   | 99WO-US05028.              |
| XX       |  |                            |
| PR       | 10-MAR-1998;   | 98US-0077450.              |
| PR       | 11-MAR-1998;   | 98US-0077632.              |
| PR       | 11-MAR-1998;   | 98US-0077641.              |
| PR       | 11-MAR-1998;   | 98US-0077649.              |
| PR       | 12-MAR-1998;   | 98US-0077791.              |
| PR       | 13-MAR-1998;   | 98US-0078004.              |
| PR       | 17-MAR-1998;   | 98US-0040220.              |
| PR       | 20-MAR-1998;   | 98US-0078886.              |
| PR       | 20-MAR-1998;   | 98US-0078910.              |
| PR       | 20-MAR-1998;   | 98US-0078936.              |
| PR       | 20-MAR-1998;   | 98US-0078939.              |
| PR       | 25-MAR-1998;   | 98US-0079294.              |

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PR 26-MAR-1998; 98US-0079656.
PR 27-MAR-1998; 98US-0079663.
PR 27-MAR-1998; 98US-0079664.
PR 27-MAR-1998; 98US-0079669.
PR 27-MAR-1998; 98US-0079728.
PR 27-MAR-1998; 98US-0079786.
PR 30-MAR-1998; 98US-0079920.
PR 30-MAR-1998; 98US-0079923.
PR 31-MAR-1998; 98US-0080105.
PR 31-MAR-1998; 98US-0080107.
PR 31-MAR-1998; 98US-0080165.
PR 31-MAR-1998; 98US-0080194.
PR 01-APR-1998; 98US-0080327.
PR 01-APR-1998; 98US-0080328.
PR 01-APR-1998; 98US-0080333.
PR 01-APR-1998; 98US-0080334.
PR 08-APR-1998; 98US-0081049.
PR 08-APR-1998; 98US-0081070.
PR 08-APR-1998; 98US-0081071.
PR 09-APR-1998; 98US-0081195.
PR 09-APR-1998; 98US-0081203.
PR 09-APR-1998; 98US-0081229.
PR 15-APR-1998; 98US-0081817.
PR 15-APR-1998; 98US-0081838.
PR 15-APR-1998; 98US-0081952.
PR 15-APR-1998; 98US-0081955.
PR 21-APR-1998; 98US-0082568.
PR 21-APR-1998; 98US-0082569.
PR 22-APR-1998; 98US-0082700.
PR 22-APR-1998; 98US-0082704.
PR 22-APR-1998; 98US-0082804.
PR 23-APR-1998; 98US-0082767.
PR 27-APR-1998; 98US-0082796.
PR 28-APR-1998; 98US-0083336.
PR 29-APR-1998; 98US-0083392.
PR 29-APR-1998; 98US-0083495.
PR 29-APR-1998; 98US-0083496.
PR 29-APR-1998; 98US-0083499.
PR 29-APR-1998; 98US-0083500.
PR 29-APR-1998; 98US-0083545.
PR 29-APR-1998; 98US-0083554.
PR 29-APR-1998; 98US-0083558.
PR 29-APR-1998; 98US-0083559.
PR 30-APR-1998; 98US-0083742.
PR 05-MAY-1998; 98US-0084366.
PR 06-MAY-1998; 98US-0084414.
PR 06-MAY-1998; 98US-0084441.
PR 07-MAY-1998; 98US-0084598.
PR 07-MAY-1998; 98US-0084600.
PR 07-MAY-1998; 98US-0084627.
PR 07-MAY-1998; 98US-0084637.
PR 07-MAY-1998; 98US-0084639.
PR 07-MAY-1998; 98US-0084640.
PR 07-MAY-1998; 98US-0084643.
PR 13-MAY-1998; 98US-0085323.
PR 13-MAY-1998; 98US-0085338.
PR 13-MAY-1998; 98US-0085339.
PR 15-MAY-1998; 98US-0085573.
PR 15-MAY-1998; 98US-0085579.
PR 15-MAY-1998; 98US-0085580.
PR 15-MAY-1998; 98US-0085582.
PR 15-MAY-1998; 98US-0085689.
PR 15-MAY-1998; 98US-0085697.
PR 15-MAY-1998; 98US-0085700.
PR 15-MAY-1998; 98US-0085704.
PR 18-MAY-1998; 98US-0086023.
PR 22-MAY-1998; 98US-0086392.
PR 22-MAY-1998; 98US-0086414.
PR 22-MAY-1998; 98US-0086430.
PR 22-MAY-1998; 98US-0086486.
PR 28-MAY-1998; 98US-0087098.
PR 28-MAY-1998; 98US-0087106.

PR 28-MAY-1998; 98US-0087208.
PR 30-JUL-1998; 98US-0094651.
PR 11-SEP-1998; 98US-0100038.
XX
PA (GETH ) GENENTECH INC.
PI Wood WI, Goddard A, Gurney A, Yuan J, Baker KP, Chen J;
XX
DR WPI; 1999-551358/46.
DR N-PSDB; AA234190.
XX
PT New secreted and transmembrane polypeptides and their polynucleotides,
PT useful for treating blood coagulation disorders, cancers and cellular
PT adhesion disorders -
XX
PS Claim 12; Fig 142; 530pp; English.
XX
CC The present invention describes secreted and transmembrane polypeptides
CC and their polynucleotides. The nucleotide sequences are useful as
CC sources of probes, primers, for chromosome mapping, and for generation
CC of antisense sequences. They can also be used to create transgenic
CC animals. The proteins can be used to treat a variety of diseases and
CC disorders, depending on their function. Diseases that may be treated
CC include blood coagulation disorders, cancers and cellular adhesion
CC disorders. They may also be used to raise antibodies. AA23391 to
CC AA24338, and AA241685 to AA241774 represent polynucleotide and
CC polypeptide sequence given in the exemplification of the present
CC invention.
XX
SQ Sequence 311 AA;

Query Match 99.6%; Score 1620; DB 20; Length 311;
Best Local Similarity 98.7%; Pred. No. 6.5e-164;
Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

QY 1 MGTFTMLEEITWTSLEMFYFALIPCLLTDEVALIPAPONLSVLTNNKHLMSPTAP 60
DB 1 mgtftmleelwtslfmffyalipclltdevaillpapnslvltnmkhlmspsvlap 60
QY 61 GETVYYSVEYGEYSLSLTSHTMIRSSMSCLTEGSECDVTDITATVPINLAVRATLSQ 120
DB 61 getvyysveygeysltshtlwipswcsltsegpcdvtditativpynlavrattlsq 120
QY 121 TSAMGILKHPFNRSITILTRPGMEIXKXGFHVIETEDIGPOFEFLVAVWXRPGAEEHY 180
DB 121 tsamgilkhpfnrstilttrpgmeltkgfhnvleiedtgpqfeflvaywrrpgaeehv 180
QY 121 tsawslkhpfnrstilttrpgmeltkgfhnvleiedtgpqfeflvaywrrpgaeehv 180
DB 181 kmvrsqgipvhletmepgaaycvkaqtfvkaigrsafegctecvevgeaipvlafaf 240
QY 181 kmvrsqgipvhletmepgaaycvkaqtfvkaigrsafegctecvevgeaipvlafaf 240
DB 181 kmvrsqgipvhletmepgaaycvkaqtfvkaigrsafegctecvevgeaipvlafaf 240
QY 241 VGFMLILVVPPLFTWKMGRLLQYSCCPVVLVLDITKITSPPKILISCREEDACATAM 300
DB 241 vgfmlilvvpplftwkmgrllqysccpvpvllditkltinspkliscreedacatavm 300
QY 301 SPEELLRAMIS 311
DB 301 speellrawis 311

RESULT 2
AAB44292
ID AAB44292 standard; Protein; 311 AA.
XX
AC AAB44292;
XX
DT 08-FEB-2001 (first entry)
XX
DE Human PRO1114 (UNQ557) protein sequence SEQ ID NO:352.
XX
KW Human; secreted protein; transmembrane protein; PRO; EST; cytosolic;
expressed sequence tag; detection; cancer.

```

```

XX Homo sapiens.
XX MO200053756-A2.
XX 14-SEP-2000.
XX 18-FEB-2000; 2000MO-US04341.
XX 08-MAR-1999; 99MO-US05028.
XX 12-MAR-1999; 99US-0123957.
XX 29-MAR-1999; 99US-0126773.
XX 21-APR-1999; 99US-0130232.
XX 28-APR-1999; 99US-0131445.
XX 14-MAY-1999; 99US-0134287.
XX 23-JUN-1999; 99US-0141037.
XX 26-JUL-1999; 99US-0145698.
XX 29-OCT-1999; 99US-0162506.
XX 30-NOV-1999; 99MO-US28313.
XX 02-DEC-1999; 99MO-US28551.
XX 16-DEC-1999; 99MO-US28565.
XX 30-DEC-1999; 99MO-US31243.
XX 30-DEC-1999; 99MO-US31274.
XX 05-JAN-2000; 2000MO-US00219.
XX 06-JAN-2000; 2000MO-US00277.
XX 06-JAN-2000; 2000MO-US00376.
XX (GETH ) GENENTECH INC.
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL,
XX Ferrara N, Fliviaroff E, Fong S, Gao W, Geber H, Gerltsen ME;
XX Godowski PJ, Grimaldi CJ, Gurney AL, Hillan KJ,
XX Kijavlin IJ, Kuo SS, Napier MA, Pan J, Paoni NF, Roy MA,
XX Shelton DL, Stewart TA, Tumas D, Williams PM, Wood WT;
XX MPI; 2000-611443/58.
XX N-PSDB; AAC78547.
XX Novel PRO polypeptides and polynucleotides used in detection methods,
XX to target bioactive molecules to specific cells, and to modulate
XX cellular activities .
XX Claim 12; Fig 142; 636pp; English.
XX AAC78458 to AAC78599 represent polynucleotide and EST (expressed
XX sequence tag) sequences which encode secreted or transmembrane PRO
XX polypeptides. The PRO polynucleotides and polypeptides have cytostatic
XX activity. The polynucleotides and polypeptides can be used for detecting
XX the presence of PRO polypeptides in samples, for linking bioactive
XX molecules to cells and for modulating biological activities of cells,
XX using the polypeptides for specific targeting. The polypeptide targeting
XX can be used to kill the target cells, e.g. for the treatment of cancers.
XX The polypeptide pairs provide specific targeting of bioactive molecules
XX to cells. AAC78600 to AAC78987 represent PCR primers and probes used in
XX the isolation of the PRO polynucleotide sequences.
XX Sequence 311 AA:

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Query Match          99.6%; Score 1620; DB 21; Length 311;
Best Local Similarity 98.7%; Pred. NO. 6.5e-164;
Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

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```

OY 1 MGFPTNMLEIWTSLFMWFYALIPCLTLDVAILPAPONTSVLSTNNKHLMSPTAP 60
    |||||||
DB 1 mgtftmyleetwslfwmffyalipclltdevallpapnslvstnnkhlmsptlap 60
    |||||||
OY 61 GEMTYIVVEYVGEYESTLTSIMIPSSKCSLTGEGECVDYTDITATVYNLRVATLSQ 120
    |||||||
DB 61 gettyvveyvgeyeslytshlwpsscsitlegpecvtditativynlrvtalsgq 120
    |||||||
OY 121 TSAWSILKHPNRNSTILTRGMEIKKGFHLVLELDLGGQFERLVAVYKREPAEEHV 180
    |||||||

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DB 121 tsawsilkhpnrstlilrpgmetckdgfhlyleledlpgqteflvayvrrpgaaehv 180
    |||||||
OY 181 KMWRSGLIVHLEETMEPGAAYCAVKAQTFVKAIXYSASFQTEVEYVGEAIPVLALFAF 240
    |||||||
DB 181 kmwrsqglivhletmepgaaycvkaqtfvkaigrasfsfscveevgeqgeipvlalfaf 240
    |||||||
OY 241 VGFMLILVVPVLFVWKMGRLLOYSCCPVVVLPDTLKITNSPORKLISCREEDACATAYM 300
    |||||||
DB 241 vgfmlilvvplfvwmkgmrgllgysccpvvvlpdtlkitnspqkliscreevdacataym 300
    |||||||
OY 301 SPEELLRAWIS 311
    |||||||
DB 301 speellrawis 311
    |||||||
RESULT 3
AAB33440
ID AAB33440 standard; Protein; 311 AA.
XX
XX AAB33440;
AC
XX
XX 29-JAN-2001 (first entry)
DT
XX
XX Human PRO1114 protein UNQ557 SEQ ID NO:144.
DE
XX
XX Human: immune related disease; diagnosis; antinflammatory; cardiant;
XX dermatological; antiarthritic; antirheumatic; immunosuppressive;
XX haemostatic; antithyroid; antidiabetic; neurotropic; neuroprotective;
XX antinaeemic; hepatotropic; virucide; antiparasitic; antiallergic;
XX antiasthmatic; systemic lupus erythematosus; rheumatoid arthritis;
XX osteoarthritis; spondyloarthropathy; systemic sclerosis; sarcoidosis;
XX idiopathic inflammatory myopathy; Sjogren's syndrome; thyroiditis;
XX systemic vasculitis; autoimmune haemolytic anaemia; diabetes mellitus;
XX autoimmune thrombocytopenia; immune-mediated renal disease;
XX demyelinating disease; hepatobiliary disease; Whipple's disease;
XX inflammatory bowel disease; gluten-sensitive enteropathy;
XX autoimmune disease; immune-mediated skin disease; allergic disease;
XX immunological disease; transplantation associated disease;
XX graft rejection; graft-versus-host-disease.
XX
XX Homo sapiens.
OS
XX
XX WO200053758-A2.
XX
XX 14-SEP-2000.
PD
XX
XX 02-MAR-2000; 2000MO-US05841.
PF
XX
XX 08-MAR-1999; 99MO-US05028.
XX 10-MAR-1999; 99US-0123618.
XX 12-MAR-1999; 99US-0123957.
XX 23-MAR-1999; 99US-0125775.
XX 12-APR-1999; 99US-0128849.
XX 20-APR-1999; 99MO-US08615.
XX 28-APR-1999; 99US-Q131445.
XX 04-MAY-1999; 99US-0132371.
XX 14-MAY-1999; 99US-0134287.
XX 02-JUN-1999; 99MO-US12252.
XX 23-JUN-1999; 99US-0141037.
XX 20-JUL-1999; 99US-0144758.
XX 26-JUL-1999; 99US-0145698.
XX 28-JUL-1999; 99US-0146222.
XX 01-SEP-1999; 99MO-US20111.
XX 08-SEP-1999; 99MO-US20594.
XX 13-SEP-1999; 99MO-US20944.
XX 15-SEP-1999; 99MO-US21090.
XX 15-SEP-1999; 99MO-US21547.
XX 05-OCT-1999; 99MO-US23089.
XX 29-OCT-1999; 99US-0162506.
XX 29-NOV-1999; 99MO-US28214.
XX 30-NOV-1999; 99MO-US28313.
XX 30-NOV-1999; 99MO-US28409.

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PR 01-DEC-1999: 99WO-US28301.
PR 01-DEC-1999: 99WO-US28634.
PR 02-DEC-1999: 99WO-US28551.
PR 02-DEC-1999: 99WO-US28564.
PR 02-DEC-1999: 99WO-US28565.
PR 16-DEC-1999: 99WO-US30095.
PR 20-DEC-1999: 99WO-US30999.
PR 30-DEC-1999: 99WO-US31274.
PR 05-JAN-2000: 2000WO-US00219.
PR 06-JAN-2000: 2000WO-US00277.
PR 06-JAN-2000: 2000WO-US00376.
PR 11-FEB-2000: 2000WO-US03565.
PR 18-FEB-2000: 2000WO-US04341.
PR 18-FEB-2000: 2000WO-US04342.
PR 22-FEB-2000: 2000WO-US04414.

(GETH ) GENENTECH INC.

Ashkenazi AJ, Baker KP, Goddard A, Gurney AL, Hebert C, Henzel W,
Kadaotf RC, Lu Y, Pan J, Pennica D, Shelton DL, Smith V,
Stewart TA, Tumas D, Watanabe CK, Wood WI, Yan M;
WPI; 2000-572271/53.
N-PSDB: AAC58605.

Sixty four PRO polypeptides, useful in the diagnosis and treatment of
immune related disorders, e.g. systemic lupus erythematosus, rheumatoid
arthritis, osteoarthritis, thyroiditis and diabetes mellitus -

Claim 33; Fig 54; 309pp; English.

The present invention describes sixty four human PRO proteins which can
be used in the treatment of immune related diseases. The human PRO
proteins, anti-PRO antibodies, agonists and antagonists are useful for
treating and diagnosing immune related disorders. The disorders are
selected from systemic lupus erythematosus, rheumatoid arthritis,
osteoarthritis, juvenile chronic arthritis, spondyloarthropathies,
systemic sclerosis, idiopathic inflammatory myopathies, Sjogren's
syndrome, systemic vasculitis, sarcoidosis, autoimmune haemolytic
anaemia, autoimmune thrombocytopenia, thyroiditis, diabetes mellitus,
immune-mediated renal disease, demyelinating diseases of the central
and peripheral nervous systems, hepatobiliary diseases, inflammatory
bowel disease, gluten-sensitive enteropathy and Whipple's disease,
autoimmune or immune-mediated skin diseases, allergic diseases,
immunological diseases of the lung, and graft-versus-host-disease.
CC diseases including graft rejection and transplant-associated
AAC58397 to AAC58578 represent PCR primers and hybridisation probes used
in the isolation of human PRO sequences. AAC58579 to AAC58642 and
AAB33414 to AAB33477 represent human PRO polynucleotide and protein
sequences given in the exemplification of the present invention.

SQ Sequence 311 AA:

```

```

Query Match          99.68; Score 1620; DB 21; Length 311;
Best Local Similarity 98.7%; Pred. No. 6.5e-164;
Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

```

OY 1 MOFTVLEIEITSLFWMFYALIPCLITDEVAILPAPONLSVSTMKHLIMSPYIAP 60
DB 1 mqfImvleieIwslImwIfyalIpcllItevalIpapnlsVstmkhlImspvIap 60
OY 61 GETVYVSVEQGESESLYTSINWIPSSWCSLTFEGPECDVDDITATVPYNLRVATGSGQ 120
DB 61 geTvYvsveqgeSeSlYtSiNwIpSsWcSlTfEGpECdVDDITATVPYNLRVatGsq 120
OY 121 TSAMSLIKHPFNNSSTILTRPGMEIKKXGFLVYLEDLGPQEFLLVYXKREPGEAHHV 180
DB 121 tsamSlIkhpfnNsStIlTrPgMEIKKxGfLVyLEdLGpQEFllVYxKRePGEAhhv 180
OY 181 KMRSGGIPVHLEETMREGAAYCYKAOITFVAIGYSAFSOTECVEVGEAIPVLALFAF 240
DB 181 kmrsggIpvHleETmREGaAYCYkAOITfVAIGySAfSOTECvEVGEaIPVLAlfAf 240

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OY 241 VGFMLILVVPVLFVWKMGRLLOYSCCPVVVLPDTLKITNSPQKLISCRREVDACATAVM 300
DB 241 vgfmlilvvpvlfvWkMgRLlOYsCCpVVVLPdTLkITnSPqKLISCRReVDaCaTAVm 300
OY 301 SPEELLRAWIS 311
DB 301 speellrawis 311

RESULT 4
AA97046
ID AA97046 standard; Protein; 311 AA.
AC AA97046;
XX
XX 31-OCT-2000 (first entry)
DE Human TANGO 242.
XX
XX TANGO 242; transmembrane; class II; cytokine receptor; chromosome 3q21;
XX cytosolic; cerebroprotective; immunomodulatory; anti-inflammatory;
XX virucide; antibacterial; vasotropic.
XX
XX Homo sapiens.
OS
XX
XX Key Location/Qualifiers
FH Peptide 1..29
FT Protein /label= Signal_peptide 30..311
FT Domain /label= Mature_protein 30..230
FT Modified-site /label= Extracellular_domain 40
FT /note= "N-linked glycosylation site" 35..125
FT Domain /label= Fibronectin_TII_domain 134
FT Modified-site /note= "N-linked glycosylation site" 231..255
FT Domain /label= Transmembrane_domain 256..311
FT Domain /label= Cytoplasmic_domain

WO200039161-A1.
XX
XX 06-JUL-2000.
XX
XX 30-DEC-1999; 99WO-US31328.
XX
XX 31-DEC-1998; 98US-0224669.
XX
XX (MILL-) MILLENNIUM PHARM INC.
XX
XX Busfield SJ;
XX
XX WPI: 2000-452372/39.
XX
XX N-PSDB: AAA51871, AAA51872.
XX
XX New nucleic acid molecules encoding polypeptides designated TANGO 241
XX and TANGO 242 used for treating e.g. brain and pancreatic disorders
XX
XX Claim 8; Fig 3; 127pp; English.
XX
XX Novel transmembrane proteins, designated TANGO 241 and TANGO 242, are
XX members of the class II cytokine receptor superfamily. The TANGO 241 and
XX 242 genes have been localized to human chromosomes 1p36 and 3q21,
XX respectively. The proteins, cDNA and their modulators can be used for the
XX treatment of viral and bacterial infection, inflammatory and autoimmune
XX disorders, vascular injury and inhibition of angiogenesis. In particular,
XX TANGO 241 can be used to treat pancreatic disorders and TANGO 242 can be
XX used to treat brain disorders.
XX

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OS Homo sapiens.  
 XX W09963088-A2.  
 XX  
 PD 09-DEC-1999.  
 XX  
 PF 02-JUN-1999; 99W0-US12252.  
 XX  
 PR 02-JUN-1998; 98US-0087607.  
 PR 02-JUN-1998; 98US-0087609.  
 PR 02-JUN-1998; 98US-0087759.  
 PR 03-JUN-1998; 98US-0087827.  
 PR 04-JUN-1998; 98US-0088021.  
 PR 04-JUN-1998; 98US-0088025.  
 PR 04-JUN-1998; 98US-0088028.  
 PR 04-JUN-1998; 98US-0088029.  
 PR 04-JUN-1998; 98US-0088030.  
 PR 04-JUN-1998; 98US-0088033.  
 PR 04-JUN-1998; 98US-0088326.  
 PR 05-JUN-1998; 98US-0088167.  
 PR 05-JUN-1998; 98US-0088202.  
 PR 05-JUN-1998; 98US-0088212.  
 PR 05-JUN-1998; 98US-0088217.  
 PR 09-JUN-1998; 98US-0088655.  
 PR 10-JUN-1998; 98US-0088722.  
 PR 10-JUN-1998; 98US-0088730.  
 PR 10-JUN-1998; 98US-0088734.  
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 PR 11-JUN-1998; 98US-0088858.  
 PR 11-JUN-1998; 98US-0088861.  
 PR 11-JUN-1998; 98US-0088863.  
 PR 11-JUN-1998; 98US-0088876.  
 PR 12-JUN-1998; 98US-0088909.  
 PR 12-JUN-1998; 98US-0089105.  
 PR 16-JUN-1998; 98US-0089440.  
 PR 16-JUN-1998; 98US-0089512.  
 PR 16-JUN-1998; 98US-0089514.  
 PR 17-JUN-1998; 98US-0089532.  
 PR 17-JUN-1998; 98US-0089538.  
 PR 17-JUN-1998; 98US-0089598.  
 PR 17-JUN-1998; 98US-0089599.  
 PR 17-JUN-1998; 98US-0089600.  
 PR 17-JUN-1998; 98US-0089653.  
 PR 18-JUN-1998; 98US-0089801.  
 PR 18-JUN-1998; 98US-0089907.  
 PR 18-JUN-1998; 98US-0089908.  
 PR 19-JUN-1998; 98US-0089947.  
 PR 19-JUN-1998; 98US-0089948.  
 PR 19-JUN-1998; 98US-0089952.  
 PR 22-JUN-1998; 98US-0090246.  
 PR 22-JUN-1998; 98US-0090252.  
 PR 22-JUN-1998; 98US-0090254.  
 PR 23-JUN-1998; 98US-0090349.  
 PR 23-JUN-1998; 98US-0090355.  
 PR 24-JUN-1998; 98US-0090429.  
 PR 24-JUN-1998; 98US-0090431.  
 PR 24-JUN-1998; 98US-0090435.  
 PR 24-JUN-1998; 98US-0090444.  
 PR 24-JUN-1998; 98US-0090445.  
 PR 24-JUN-1998; 98US-0090461.  
 PR 24-JUN-1998; 98US-0090472.  
 PR 24-JUN-1998; 98US-0090535.  
 PR 24-JUN-1998; 98US-0090538.  
 PR 24-JUN-1998; 98US-0090540.  
 PR 24-JUN-1998; 98US-0090557.

PR 25-JUN-1998; 98US-0090676.  
 PR 25-JUN-1998; 98US-0090678.  
 PR 25-JUN-1998; 98US-0090688.  
 PR 25-JUN-1998; 98US-0090690.  
 PR 25-JUN-1998; 98US-0090691.  
 PR 25-JUN-1998; 98US-0090694.  
 PR 25-JUN-1998; 98US-0090695.  
 PR 25-JUN-1998; 98US-0090696.  
 PR 26-JUN-1998; 98US-0090682.  
 PR 01-JUL-1998; 98US-0091360.  
 PR 01-JUL-1998; 98US-0091360.  
 PR 01-JUL-1998; 98US-0091364.  
 PR 02-JUL-1998; 98US-0091478.  
 PR 02-JUL-1998; 98US-0091486.  
 PR 02-JUL-1998; 98US-0091519.  
 PR 02-JUL-1998; 98US-0091626.  
 PR 02-JUL-1998; 98US-0091628.  
 PR 02-JUL-1998; 98US-0091633.  
 PR 02-JUL-1998; 98US-0091646.  
 PR 02-JUL-1998; 98US-0091673.  
 PR 07-JUL-1998; 98US-0091678.  
 PR 07-JUL-1998; 98US-0091982.  
 PR 09-JUL-1998; 98US-0092182.  
 PR 10-JUL-1998; 98US-0092472.  
 PR 20-JUL-1998; 98US-0093339.  
 PR 30-JUL-1998; 98US-0094651.  
 PR 04-AUG-1998; 98US-0095282.  
 PR 04-AUG-1998; 98US-0095285.  
 PR 04-AUG-1998; 98US-0095301.  
 PR 04-AUG-1998; 98US-0095302.  
 PR 04-AUG-1998; 98US-0095318.  
 PR 04-AUG-1998; 98US-0095321.  
 PR 04-AUG-1998; 98US-0095325.  
 PR 10-AUG-1998; 98US-0095916.  
 PR 10-AUG-1998; 98US-0095929.  
 PR 10-AUG-1998; 98US-0096012.  
 PR 11-AUG-1998; 98US-0096143.  
 PR 11-AUG-1998; 98US-0096146.  
 PR 12-AUG-1998; 98US-0096329.  
 PR 17-AUG-1998; 98US-0096757.  
 PR 17-AUG-1998; 98US-0096766.  
 PR 17-AUG-1998; 98US-0096768.  
 PR 17-AUG-1998; 98US-0096773.  
 PR 17-AUG-1998; 98US-0096791.  
 PR 17-AUG-1998; 98US-0096867.  
 PR 17-AUG-1998; 98US-0096891.  
 PR 17-AUG-1998; 98US-0096894.  
 PR 17-AUG-1998; 98US-0096895.  
 PR 17-AUG-1998; 98US-0096897.  
 PR 18-AUG-1998; 98US-0096949.  
 PR 18-AUG-1998; 98US-0096950.  
 PR 18-AUG-1998; 98US-0096959.  
 PR 18-AUG-1998; 98US-0096960.  
 PR 18-AUG-1998; 98US-0097022.  
 PR 19-AUG-1998; 98US-0097141.  
 PR 20-AUG-1998; 98US-0097218.  
 PR 24-AUG-1998; 98US-0097661.  
 PR 26-AUG-1998; 98US-0097951.  
 PR 26-AUG-1998; 98US-0097952.  
 PR 26-AUG-1998; 98US-0097954.  
 PR 26-AUG-1998; 98US-0097955.  
 PR 26-AUG-1998; 98US-0097971.  
 PR 26-AUG-1998; 98US-0097974.  
 PR 26-AUG-1998; 98US-0097978.  
 PR 26-AUG-1998; 98US-0097979.  
 PR 26-AUG-1998; 98US-0097986.  
 PR 26-AUG-1998; 98US-0098014.  
 PR 31-AUG-1998; 98US-0098525.  
 PR 16-SEP-1998; 98US-0100634.  
 PR 12-JAN-1999; 99US-0115565.  
 XX  
 PA (GETH ) GENENTECH INC.

|                           |   |
|---------------------------|---|
| XX                        | Baker K, Chen J, Goddard A, Gurney AL, Smith V, Watanabe CK;              |
| PI                        | Wood WJ, Yuan J;  |
| XX                        | WPI; 2000-072883/06.  |
| DR                        | N-PSDB; AA265011.   |
| XX                        | Membrane-bound proteins and related nucleotide sequences                  |
| PT                        | claim 12; Fig 117; 822pp; English.  |
| XX                        |   |
| PS                        | The invention provides membrane-bound PRO polypeptides and                |
| CC                        | polynucleotides encoding them. The PRO sequences of the invention were    |
| CC                        | identified based on extracellular domain homology screening. The PRO      |
| CC                        | sequences have homology with proteins including LDL receptors, TIE        |
| CC                        | ligands and various enzymes. The membrane-bound proteins and receptor     |
| CC                        | molecules are useful as pharmaceutical and diagnostic agents. Receptor    |
| CC                        | immunohistins, for instance, can be used as therapeutic agents to block   |
| CC                        | receptor-ligand interactions. The membrane-bound proteins can also be     |
| CC                        | employed for screening of potential peptide or small molecule inhibitors  |
| CC                        | of the relevant receptor/ligand interaction. The PRO encoding sequences   |
| CC                        | are useful as hybridization probes, in chromosome and gene mapping and in |
| CC                        | the generation of antisense RNA and DNA. PRO nucleic acid sequences       |
| CC                        | will also be useful for the preparation of PRO polypeptides, especially   |
| CC                        | by recombinant techniques.  |
| XX                        |   |
| SO                        | Sequence 311 AA;  |
| Query Match               | 99.6%; Score 1620; DB 21; Length 311;                                     |
| Best Local Similarity     | 98.7%; Pred. No. 6-5e-164;  |
| Matches 307; Conservative | 0; Mismatches 4; Indels 0; Gaps 0   |
| OY                        | 1 MQTFTVLEELTSLPMMFFVALICLLTDEVAIIIPAPONLSVLTNKHLMMSVIAIP 60              |
| DB                        | 1 mqtftvleelstslfpmffyalipclldevalipapnqslvstnmkhllmwspsviap 60           |
| OY                        | 61 GETVYVSYVEQGEYSILVSHTWISSMCSLREGPCDVTDDITAVPNLAVRATLGSQ 120            |
| DB                        | 61 getvyvsveyqgeysilvshwipsswsclslegpcdvtdditavpnlvratlgsq 120            |
| OY                        | 121 TSAWSILKHPRFNRTIILRPGMEILKXKGFHLVIELEDGPOPEFLVAVWXRPGAEHY 180         |
| DB                        | 121 tsawsilkhprfnrtiilrpgmelktgfnhlvleledgppqfeflvaywrrpgaeen 180         |
| OY                        | 181 KMWNSGGLPVLHETMPCGAAYCVKAQTEVKAIGXYSAFSQTECEVQGAIPLVLAFAF 240         |
| DB                        | 181 kmwrsrgglpvlhetmpgaaaycvkaqtefkaigrxysafsqteceveqgaipvlalaf 240       |
| OY                        | 241 VQFMILIVVPLFLVWKMGBLLQYSCPPVVLBDTLKITNSPQKLISGREEDVACTATM 300         |
| DB                        | 241 vqfmilivvplflvwkmgrllqysccpvpvlpdtklilnspkllisctreevadacatam 300      |
| OY                        | 301 SPEELLRAWIS 311   |
| DB                        | 301 speellrawis 311   |
| RESULT 7                  |   |
| AAAB65199                 |   |
| ID                        | AAAB65199 standard; Protein; 311 AA.                                      |
| XX                        |   |
| AC                        | AAAB65199;  |
| XX                        |   |
| DT                        | 02-APR-2001 (first entry)   |
| XX                        |   |
| DE                        | Human PRO1114 (UNQ557) protein sequence SEQ ID NO:183.                    |
| XX                        |   |
| KW                        | Human; secreted and transmembrane protein; PRO; cytosolic;                |
| KW                        | cell death; cancer; chromosomal mapping; gene mapping; tissue typing;     |
| XX                        | diagnostic assay.   |
| XX                        |   |
| OS                        | Homo sapiens.   |

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XX PN WO200073454-A1.
XX PD
XX 07-DEC-2000.
XX PF
XX 30-MAR-2000; 2000OWO-US08439.
XX
PR 02-JUN-1999; 99WO-US12252.
PR 23-JUN-1999; 99US-0141037.
PR 07-JUL-1999; 99US-0143048.
PR 20-JUL-1999; 99US-0144758.
PR 26-JUL-1999; 99US-0145698.
PR 18-JUL-1999; 99US-0146222.
PR 17-AUG-1999; 99US-0149366.
PR 15-SEP-1999; 99WO-US21090.
PR 15-SEP-1999; 99WO-US21547.
PR 08-OCT-1999; 99US-0158663.
PR 30-NOV-1999; 99WO-US28313.
PR 01-DEC-1999; 99WO-US28301.
PR 16-DEC-1999; 99WO-US30095.
PR 20-DEC-1999; 99WO-US30911.
PR 05-JAN-2000; 2000OWO-US00219.
PR 06-JAN-2000; 2000OWO-US00376.
PR 11-FEB-2000; 2000OWO-US03565.
PR 18-FEB-2000; 2000OWO-US04341.
PR 22-FEB-2000; 2000OWO-US04414.
PR 24-FEB-2000; 2000OWO-US04914.
PR 24-FEB-2000; 2000OWO-US05004.
PR 02-MAR-2000; 2000OWO-US05841.
PR 15-MAR-2000; 2000OWO-US06884.
PR 20-MAR-2000; 2000OWO-US07377.
XX
XX (GETH ) GENENTECH INC.
XX PA
XX Ashkenazi AJ, Baker KP, Botstein D, Desnoyers L, Eaton DL;
XX Ferrera N, Fong S, Geber H, Gerlitsen ME, Goddard A, Godowski PJ;
XX Grimaldi CJ, Gunney AL, Kljavin IJ, Napier MA, Pan J, Paoni NF;
XX Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PM, Wood WJ;
XX Zhang Z;
XX
XX WPI; 2001-032160/04.
XX DR N-PSDB; AAF44157.
XX
XX PRO polynucleotides used to produce polypeptides used to target
XX PT bioactive molecules such as toxins, radiolabels or antibodies, to
XX PT specific cells, to cause targeted cell death -
XX
XX Claim 12; Fig 117; 935pp; English.
XX
XX The present invention describes human secreted and transmembrane PRO
XX CC proteins. The PRO proteins have cytosstatic activity. The PRO proteins
XX CC can be used for targeted delivery of bioactive molecules, such as
XX CC toxins, radiolabels or antibodies, that cause cell death. PRO nucleotide
XX CC sequences, and their fragments, can be used as hybridisation probes, in
XX CC chromosomal and gene mapping, and in the generation of anti-sense RNA
XX CC and DNA. They may also be used to produce transgenic animals which are
XX CC used to develop and screen therapeutically useful reagents. The PRO
XX CC nucleotide and protein sequence can be used for tissue typing and in
XX CC treating cancer. Anti-PRO antibodies can be used in diagnostic assays.
XX CC AAF44270 to AAF44470 represent PCR primers and hybridisation probes used
XX CC in the isolation of human PRO sequences. AAF44087 to AAF44269 and
XX CC AAB65154 to AAB65300 represent human PRO polynucleotide and protein
XX CC sequences given in the exemplification of the present invention.
XX
XX Sequence 311 AA:
XX
XX Query Match 99.6%; Score 1620; DB 22; Length 311;
XX Best Local Similarity 98.7%; Pred. No. 6.5e-16;
XX Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;
XX
XX 1 MOTFMVLEETITSLFMFFVALIICLLTDEVAIILPAPQNLVSLSTNMKHLMMSPVIAP 60
XX |

```



```

Db      1 mgtftmveeiwtstlfmwfyyalipclltdevallpapqnlsvlstnmkhlmspvap 60
QY      61 GETVYVSEYEGEESLYTSHTIMIPSSWCSLTGEGPCDVTDDITATVPYNLRVRATLGSQ 120
        |||
Db      61 getvyysegyegeslytshtlwpsswcsltegpedvdditativynlrvatlgsq 120
QY      121 TSAMSLIKHPENRSTILTRPGMEIKKXGPHLYIELEDLGPOFEFLVAYXKREGAEHV 180
        |||
Db      121 tsawslkhpnstliltrpgmekdghlyleledlgpqfelfvayvrpgaehev 180
QY      181 KMWRSGLIPVHLETMEPGAAYCVKAOTFVKAIGXSAFSQTECEVVGGEALPVLALFAF 240
        |||
Db      181 kmvrsqgipvhletmepgaaycvkaqtfvkaigrsafsqtecevggealplvialfaf 240
QY      241 VGFMILVWPVPLFWMKGRLLQYSCCPVVVLPDTLKITNSPORKLISCRREVDACATAVM 300
        |||
Db      241 vgfmllvwpplfwkmgrllqysccpvvvlpdtlkitnspqkliscreevdacatavm 300
        |||
        301 SPEELLRAWIS 311
        |||
        301 speellrawis 311

```

## RESULT 8

AA939472 ID AAY39472 standard; Protein; 311 AA.

AC AAY39472;

DT 19-NOV-1999 (first entry)

DE DNAX Interferon-like receptor subunit 1 protein sequence.

KM DNAX interferon-like receptor subunit; DIRS1; DIRS2; cytokine receptor; therapy; degenerative condition; abnormal condition; cellular development; cell differentiation.

XX Homo sapiens.

OS WO9946379-A2.

PN 16-SEP-1999.

PD 08-MAR-1999; 99WO-US03735.

PF 09-MAR-1998; 98US-0037394.

PR (SCHE ) SCHERING CORP.

PI Parham CL, Moore KW, Murgolo NJ, Bazan JF;

DR WPI; 1999-551408/46.

DR N-PSDB; AAZ20504.

XX New receptor subunits potentially useful, e.g. for treating degenerative and abnormal conditions that involve cellular development,

PT Claim 1; Page 74-76; 82pp; English.

CC This sequence is the DNAX Interferon-like receptor subunit 1 (DIRS1) of the invention. The invention also relates to the DIRS2 protein sequence. The DIRS1 and DIRS2 sequences are subunits of receptors related to cytokine receptors. The isolated receptor gene provides means to generate an economical source of the receptor, allow expression of more receptors on a cell leading to increased assay sensitivity, promote characterization of various receptor subtypes and variants, and allow correlation of activity with receptor structures. The invention should contribute to new therapies for degenerative and abnormal conditions that involve cellular development, differentiation or function.

XX Sequence 311 AA.

Query Match 99.5%; Score 1619; DB 20; Length 311;  
Best Local Similarity 98.7%; Pred. No. 8.3e-164;  
Matches 307; Conservative 0; Mismatches 4; Indels 0; Gaps 0;

```

QY      1 MGTFTMVEEITSLTFMWFYALIPCLLTDEVALIPAPQNLVSVLSTNMKHLMSPVAP 60
        |||
Db      1 mgtftmveeiwtstlfmwfyyalipclltdevallpapqnlsvlstnmkhlmspvap 60
QY      61 GETVYVSEYEGEESLYTSHTIMIPSSWCSLTGEGPCDVTDDITATVPYNLRVRATLGSQ 120
        |||
Db      61 getvyysegyegeslytshtlwpsswcsltegpedvdditativynlrvatlgsq 120
QY      121 TSAMSLIKHPENRSTILTRPGMEIKKXGPHLYIELEDLGPOFEFLVAYXKREGAEHV 180
        |||
Db      121 tsawslkhpnstliltrpgmekdghlyleledlgpqfelfvayvrpgaehev 180
QY      181 KMWRSGLIPVHLETMEPGAAYCVKAOTFVKAIGXSAFSQTECEVVGGEALPVLALFAF 240
        |||
Db      181 kmvrsqgipvhletmepgaaycvkaqtfvkaigrsafsqtecevggealplvialfaf 240
QY      241 VGFMILVWPVPLFWMKGRLLQYSCCPVVVLPDTLKITNSPORKLISCRREVDACATAVM 300
        |||
Db      241 vgfmllvwpplfwkmgrllqysccpvvvlpdtlkitnspqkliscreevdacatavm 300
QY      301 SPEELLRAWIS 311
        |||
Db      301 speellrawis 311

```

## RESULT 9

AA97048 ID AAY97048 standard; Protein; 308 AA.

AC AAY97048;

DT 31-OCT-2000 (first entry)

DE Murine TANGO 242.

KM TANGO 242; transmembrane; class II; cytokine receptor; cytostatic; cerebroprotective; immunomodulatory; anti-inflammatory; virocidic;

KW antibacterial; vasotropic.

XX Mus sp.

PN WO200039161-A1.

PD 06-JUL-2000.

PF 30-DEC-1999; 99WO-US31328.

PR 31-DEC-1998; 98US-0224669.

PA (MILL-) MILLENNIUM PHARM INC.

PI Busfield SJ;

DR WPI; 2000-452372/39.

DR N-PSDB; AAA51875, AAA51876.

XX New nucleic acid molecules encoding polypeptides designated TANGO 241 and TANGO 242 used for treating e.g. brain and pancreatic disorders

PS Disclosure; Fig 8A-B; 127pp; English.

CC Novel transmembrane proteins, designated TANGO 241 and TANGO 242, are members of the class II cytokine receptor superfamily. The TANGO 241 and 242 genes have been localized to human chromosomes 1p36 and 3q21, respectively. The proteins, cDNA and their modulators can be used for the treatment of viral and bacterial infection, inflammatory and autoimmune disorders, vascular injury and inhibition of angiogenesis. In particular, TANGO 241 can be used to treat pancreatic disorders and TANGO 242 can be



CC viruses, bacteria and parasites (especially intracellular pathogens) and  
 CC for preventing organ rejection. A vector containing (1) is used to  
 CC restore, e.g. by gene therapy, IL-10 sensitivity to a cell that expresses  
 CC a dysfunctional IL10R and is able to bind IL-10 but not to transduce a  
 CC signal. Antisense CRF4 sequences (especially ribozymes), can inhibit  
 CC IL-10 activity in cells. Antibodies specific for CRF4 are used to  
 CC measure and localise CRF4, for diagnosis of defective IL-10 activity.  
 CC Fragments of (1) are used as primers or probes to assay CRF4-specific  
 CC RNA. Agonists/antagonists may be administered parenterally, orally or  
 CC rectally especially by intravenous injection or directly into a tumour or  
 CC allograft.

CC Sequence 325 AA:

Query Match 11.7%; Score 191; DB 19; Length 325;

Best Local Similarity 26.6%; Pred. No. 6,2e-12;  
 Matches 77; Conservative 47; Mismatches 117; Indels 48; Gaps 16;

12 WTSLEMFYALIPCLTDEVALIPAPONLSVLTSMKHLMM-SPVIAPEYVYSEY 70

3 W-SIGSV---LGGCLLSALGMVPPENVYRMSVNFKNILQWESPATAG-----NLTf 52

71 QGEYSLYTSHIWPSSMCSITEGECDDVDITATVPYNLRVATLGSQTSAM-SILKH 129

53 taqlysyf-----lfqdkmnlitlcedfs-slskygqhlrtvraefadshdwntlfc 106

130 PFNPNSTILTRPGMEIKKXGFHLVLEEDLGPQFE-----FLVAYMXRE 173

107 pv--ddllppgmqvevladsl--hmrflapkleneyetuknynswtynqyw--k 160

174 PGAEHVMKVRSGIPVHLETFMGACVCAKQTFVKAIGXYSFSGTECV-VOGEAIP 232

161 ngtlekfgitpdyqfey-lrnlepwtcyvgrglpdrnkagsepevcqthdelpv 219

233 ---LVLLFAVFGMLIVVPLF--VWKGRLQYSCCPVVLPTDK 276

220 smmvaavilmasv-fmvtallgcfslwcykktkylatsprnsipqhlk 267

DB

RESULT 12  
 AAB31214

AAB31214 standard; Protein: 325 AA.

AC AAB31214;

XX 20-APR-2001 (first entry)

XX Amino acid sequence of human polypeptide PRO2630.

XX Human; secreted protein; transmembrane protein; PRO196; PRO444; PRO183;

XX PRO185; PRO210; PRO215; PRO217; PRO242; PRO288; PRO365; PRO1361; PRO1308;

XX PRO1183; PRO1272; PRO1419; PRO1499; PRO1710; PRO248; PRO353; PRO1318;

XX PRO1600; PRO333; PRO337; PRO337; PRO337; PRO337; PRO337; PRO337; PRO337;

XX PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630;

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XX PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630;

XX PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630;

XX PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630;

FT Domain /note= "N-glycosylation site"  
 FT 222..245  
 FT /note= "transmembrane domain"  
 FT 316..322  
 FT /note= "N-myristoylation site"

PN WO200077037-A2.

PD 21-DEC-2000.

XX 22-MAY-2000; 2000WO-US14042.

XX 15-JUN-1999; 99US-0139695.

XX 20-JUL-1999; 99US-0145070.

XX 26-JUL-1999; 99US-0145698.

XX 17-AUG-1999; 99US-0149396.

XX 01-SEP-1999; 99WO-US20111.

XX 08-SEP-1999; 99WO-US20594.

XX 15-SEP-1999; 99WO-US21090.

XX 30-NOV-1999; 99WO-US28313.

XX 01-DEC-1999; 99WO-US28301.

XX 02-DEC-1999; 99WO-US28565.

XX 07-DEC-1999; 99US-0169495.

XX 05-JAN-2000; 2000WO-US00219.

XX 18-FEB-2000; 2000WO-US04341.

XX 18-FEB-2000; 2000WO-US04342.

XX 22-FEB-2000; 2000WO-US04414.

XX 01-MAR-2000; 2000WO-US05601.

XX 02-MAR-2000; 2000WO-US05841.

XX 20-MAR-2000; 2000WO-US07377.

XX 30-MAR-2000; 2000WO-US08439.

XX 15-MAY-2000; 2000WO-US13358.

XX 17-MAY-2000; 2000WO-US13705.

XX (GENE ) GENENTECH INC.

XX Ashkenazi AJ, Baker KP, Bolstein DA, Desnoyers L, Eaton DL;

XX Ferrara N, Fong S, Gao W, Gerber H, Gerritsen ME, Goddard A;

XX Godowski PJ, Gurney AJ, Kljavin IJ, Mather JP, Napier MA, Pan J;

XX Paoni NF, Roy MA, Stewart TA, Tumas D, Watanabe CK, Williams PW;

XX Wood WJ, Zhang Z;

XX WPI: 2001-050091/06.

XX N-PSDB; AAC87060.

XX Isolated nucleic acid molecule encoding a PRO polypeptide which is a

XX transmembrane polypeptide is useful for gene therapy and identification

XX of related polypeptides -

XX Claim 12; Fig 72; 244pp; English.

XX The present sequence represents a human secreted and transmembrane

XX polypeptide. The specification describes human polypeptides, designated

XX PRO196, PRO444, PRO183, PRO210, PRO215, PRO217, PRO242, PRO288,

XX PRO365, PRO1361, PRO1308, PRO1183, PRO1272, PRO1419, PRO1499, PRO1710,

XX PRO248, PRO353, PRO337, PRO337, PRO337, PRO337, PRO337, PRO337, PRO337;

XX PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630;

XX PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630;

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XX PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630;

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XX PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630;

XX PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630; PRO2630;



```

QY 69 EYGEVESLSTSHWIPSSMCSTEGPCDVTDTATVP-----YMLRATIGS 119
Db 66 qfytstskwtadmsigvncitqitatec-----dfiaapsagfpmdfnvlrtraelga 121
QY 120 OTSAMSIL---KHPFNNSSTILTRPGMEIKKXGFHLVI-----ELDLGPQFE-PLVAY 169
Db 122 lhaawtumpvfgn--yrnvvtvgppenievppgegsllilrfspidictatfcygvhy 179
QY 170 WAREPGAEEHVK-MVRSGGIPVHLETPMGAAYCVKAQ-----TFVKAIGXSAFSQT 221
Db 180 w--ekgigqvkqpfirsnsi--sldnlkpsrvcyqlqvgaqlmknknllfrvghlns-- 233
QY 222 ECEVEGCEA-IPVLALFARVGFMLILVVP-----LFWMKGRLLQY 263
Db 234 -cydlnadaastelqvllsvgtflslsvlagacflvlkyrgllyk 279

```

RESULT 15

28496 AAR28496 standard; Protein; 557 AA.

XX AAR28496;

DT 31-MAR-1993 (first entry)

DE Sequence of a soluble form of the interferon (IFN) receptor  
with a high affinity for IFN-alpha and -beta.

DE Interferon receptor; alpha-interferon; beta-interferon.

OS Synthetic.

XX WO9218626-A.

PD 29-OCT-1992.

PF 17-APR-1991: 91WO-FR00318.

PR 17-APR-1991: 91WO-FR00318.

PA (EUBI-) LAB EURO BIOTECHNOLOGIE.

XX Eid P, Gresser I, Lutfalla G, Meyer F, Mogensen KE;

PI Tovey M, Uze G;

XX MPI; 1992-382110/46.

DR N-PSDB; AAQ30533.

PT Water soluble polypeptide(s) strongly bind interferon(s) alpha  
and beta - useful as immunosuppressants, for treating auto-immune  
diseases and transplant rejection

PS Claim 3; Fig 2; 58pp; English.

CC DNA encoding the water-soluble polypeptide with a high affinity for  
CC IFN-alpha and -beta is isolated by PCR, using appropriate  
CC oligonucleotides as primers and cloned cDNA as template. For example,  
CC bacteriophage lambda ZAP, containing the entire coding sequence of  
CC the IFN-alpha and -beta receptor (AAQ30533), was incubated with oligos  
CC AAQ30534 and AAQ30535. AAR28496 represents the complete receptor.  
CC AAR28495 lacks the transmembrane and cytoplasmic domains. Both forms  
CC bind IFN in the same way as antibodies so are immunosuppressants e.g.  
CC for treating autoimmune diseases and graft rejection. They lack the  
CC toxic side-effects of known immunosuppressants such as steroids.

XX Sequence 557 AA;

```

QY 21 YALITCLTDEVAIIPAPQNLSTNMKHLMSPIAPCTVYYSVEYGEYSLT- 79
Db 215 yspvhcixktvenelpppenlevsqnqnylkw-----dytannmfqyqwlhafilx 267
QY 80 ---SHWIPSSMCSTEGPCDVTDTATVPVN-----LVRATIGSQTAMS- 125
Db 268 rnpqnily---kwqdl---pdceuvktqcvfpqnvfqkyllyllrvqasdgntsfwsee 321
QY 126 -----LKHPFNNSSTILTRPGMEIKKXGFHLVI-----ELDLGPQFEF 165
Db 322 ikfdeiqafllppvfnlrs-----lsdsfhiyigapkgsgnprvldqpllye- 370
QY 166 LVATWAREPGAEEHVKMVRSGGIPVHLETPMGAAYCVKAQ--TFVKAIGXSAFSQTEC 223
Db 371 -lftwensnaerklietkt--dvtvpnlkpltyvcvkarahndeklnksvfsdave 426
QY 224 VEVO-GEAIPVLALFARVGFMLILVVPPLFVWMKGRLLQYSCCVVVLPRDLKXTNS- 280
Db 427 ektpqntsklwl-----lvglciafaipfvlyaaaklfr--clnyviffr-slkpsssid 479
QY 281 -----PQR--LISCREEVDAC 295
Db 480 eyfseqplknlllstseeqiekc 502

```

Search completed: October 12, 2001, 16:09:56  
Job time: 188 sec

Query Match 10.0%; Score 163.5; DB 13; Length 557;  
Best Local Similarity 22.0%; Pred. No. 1.1e-08;  
Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;



GenCore version 4.5  
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OM protein - protein search, using sw model

Run on: October 12, 2001, 16:09:33 ; Search time 11.2 Seconds

(without alignments)  
951.201 Million cell updates/sec

Title: US-09-265-540e-2

Perfect score: 1627  
Sequence: 1 MDTFTVLEIEITWTLFWMF.....VDACATVMSPEELRAMIS 311

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 93435 seqs, 34255486 residues

Total number of hits satisfying chosen parameters: 93435

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Database : SwissProt\_39:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

## SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description        |
|------------|-------|-------------|--------|----|--------------------|
| 1          | 191   | 11.7        | 325    | 1  | Q08334 homo sapien |
| 2          | 178.5 | 11.0        | 337    | 1  | ING5_HUMAN         |
| 3          | 178.5 | 11.0        | 590    | 1  | INR1_MOUSE         |
| 4          | 170.5 | 10.5        | 349    | 1  | 1105_MOUSE         |
| 5          | 164.5 | 10.1        | 560    | 1  | INR1_BOVIN         |
| 6          | 162.5 | 10.0        | 557    | 1  | INR1_HUMAN         |
| 7          | 157.5 | 9.7         | 560    | 1  | INR1_SHEEP         |
| 8          | 136   | 8.4         | 578    | 1  | 110R_HUMAN         |
| 9          | 130   | 8.0         | 292    | 1  | TE_RABIT           |
| 10         | 125.5 | 7.7         | 295    | 1  | TE_HUMAN           |
| 11         | 125.5 | 7.7         | 575    | 1  | 110R_MOUSE         |
| 12         | 121.5 | 7.5         | 289    | 1  | TE_CAVPO           |
| 13         | 121   | 7.4         | 489    | 1  | INGR_HUMAN         |
| 14         | 119.5 | 7.3         | 294    | 1  | TE_MOUSE           |
| 15         | 114.5 | 7.0         | 292    | 1  | TE_BOVIN           |
| 16         | 114   | 7.0         | 295    | 1  | TE_RAT             |
| 17         | 114   | 7.0         | 507    | 1  | EPOR_MOUSE         |
| 18         | 99    | 6.1         | 507    | 1  | EPOR_RAT           |
| 19         | 97    | 6.0         | 508    | 1  | EPOR_HUMAN         |
| 20         | 96    | 5.9         | 984    | 1  | EPB1_HUMAN         |
| 21         | 96    | 5.9         | 984    | 1  | EPB1_RAT           |
| 22         | 96    | 5.9         | 1447   | 1  | DCX_MOUSE          |
| 23         | 95    | 5.8         | 1447   | 1  | DCX_HUMAN          |
| 24         | 92.5  | 5.7         | 987    | 1  | EPB4_HUMAN         |
| 25         | 89    | 5.5         | 831    | 1  | PRLR_CHICK         |
| 26         | 89    | 5.5         | 977    | 1  | EPB2_MOUSE         |
| 27         | 88.5  | 5.4         | 1928   | 1  | LRP_RAT            |
| 28         | 88    | 5.4         | 902    | 1  | EPBB_XENLA         |
| 29         | 88    | 5.4         | 985    | 1  | EPAB_XENLA         |
| 30         | 87    | 5.3         | 984    | 1  | EPB1_CHICK         |
| 31         | 86    | 5.3         | 227    | 1  | COX2_HAPGR         |
| 32         | 86    | 5.3         | 227    | 1  | COX2_LYCP1         |
| 33         | 86    | 5.3         | 227    | 1  | COX2_RABIT         |

|    |      |     |      |   |            |                    |
|----|------|-----|------|---|------------|--------------------|
| 34 | 86   | 5.3 | 379  | 1 | COS4_YEAST | P43542 saccharomyc |
| 35 | 85.5 | 5.3 | 1630 | 1 | PTPL_DROME | P35992 drosophila  |
| 36 | 85   | 5.2 | 227  | 1 | COS2_CERS1 | P03851 ceratotheri |
| 37 | 85   | 5.2 | 227  | 1 | COS2_DAMP  | P50679 damalisus   |
| 38 | 85   | 5.2 | 227  | 1 | COS2_RHIN  | O96190 rhinoceros  |
| 39 | 85   | 5.2 | 227  | 1 | COS2_SHEEP | O78750 ovine       |
| 40 | 84.5 | 5.2 | 862  | 1 | 1125_HUMAN | O99665 homo sapien |
| 41 | 84   | 5.2 | 227  | 1 | COS2_GAPI  | O37430 capra hircu |
| 42 | 84   | 5.2 | 227  | 1 | COS2_EQUAS | P92478 equus asinu |
| 43 | 84   | 5.2 | 227  | 1 | COS2_HORSE | P48660 equus cabal |
| 44 | 84   | 5.2 | 227  | 1 | COS2_MACRO | P92662 macropus ro |
| 45 | 84   | 5.2 | 227  | 1 | COS2_PROTA | P98042 propithecus |

## ALIGNMENTS

```

RESULT 1
ID      1105_HUMAN
AC      008334;
DT      01-FEB-1995 (Rel. 31, Created)
DT      01-FEB-1995 (Rel. 31, Last sequence update)
DT      01-OCT-2000 (Rel. 40, Last annotation update)
DE      INTERLEUKIN-10 RECEPTOR BETA CHAIN PRECURSOR (IL-10R-B) (IL-10R2)
DE      (CYTOKINE RECEPTOR CLASS-II CRF2-4).
GN      IL10RB OR CRFB4.
OS      Homo sapiens (Human).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
OX      NCBI_TaxID=9606;
RN      [1]
RP      TISSUE=Retal brain;
RX      MEDLINE=93300510; PubMed=8314576;
RA      Lutfalla G., Gardiner K., Uze G.;
RT      *A new member of the cytokine receptor gene family maps on chromosome
RT      21 at less than 35 kb from IFNAR.
RL      Genomics 16:366-373(1993).
RN      [2]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=96054036; PubMed=7563119;
RA      Lutfalla G., McInnis M.G., Antonarakis S.E., Uze G.;
RT      *Structure of the human CRFB4 gene: comparison with its IFNAR
RT      neighbor.
RL      J. Mol. Evol. 41:338-344(1995).
RN      [3]
RP      CHARACTERIZATION.
RX      MEDLINE=97459974; PubMed=9312047;
RA      Kotenko S.V., Krause C.D., Izotova L.S., Pollack B.P., Wu W.,
RA      Pestka S.;
RT      *Identification and functional characterization of a second chain of
RT      the interleukin-10 receptor complex.
RL      EMBO J. 16:5894-5903(1997).
CC      -1- FUNCTION: RECEPTOR FOR IL-10. SERVES AS AN ACCESSORY CHAIN
CC      ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO INITIATE
CC      IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.
CC      -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC      -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC      -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC      This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC      the European Bioinformatics Institute. There are no restrictions on its
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CC      modified and this statement is not removed. Usage by and for commercial
CC      entities requires a license agreement (See http://www.isb-stb.ch/announce/
CC      or send an email to license@isb-stb.ch).
CC      EMBL, 217227; CAA78933.1;
CC      EMBL, 008988; AAA86872.1;
CC      PIR: A47003; A47003.
CC      HSSP: P13726; IDAN.

```

DR MIM: 123889; -  
 KM Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 19 POTENTIAL.  
 FT CHAIN 20 325 INTERLEUKIN-10 RECEPTOR BETA CHAIN.  
 FT DOMAIN 20 325 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 221 242 POTENTIAL.  
 FT DOMAIN 243 325 CYTOPLASMIC (POTENTIAL).  
 FT DOMAIN 113 205 FIBRONECTIN TYPE-III.  
 FT DISULFID 66 74 BY SIMILARITY.  
 FT DISULFID 188 209 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 49 49 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 68 68 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 102 102 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 161 161 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CONFLICT 124 124 A -> D (IN REF. 2).  
 FT CONFLICT 269 273 FLAGHP -> VGRME (IN REF. 2).  
 FT CONFLICT 274 325 MISSING (IN REF. 2).  
 SO SEQUENCE 325 AA; 37011 MM; 66706C79F8514B23 CRC64;

Query Match 11.7%; Score 191; DB 1; Length 325;  
 Best Local Similarity 26.6%; Pred. No. 8e-10;  
 Matches 77; Conservative 47; Mismatches 117; Indels 48; Gaps 16;

QY 12 WTSLEFMWFFALLPCULTDEVALIPAPONLSVSTNKKHLLMW-SPIYAFGEITYYSEY 70  
 DB 3 W-SLGSW---LGGCLLSVALGAVPPEENVNMSVNFKNILQWSPAFAGK-----NLTF 52  
 QY 71 QGEYESLYTSHWIPSSWCSLTGEGPCDVDDITATVPYNLRATLGSQTSAM-SILKH 129  
 DB 53 TAOYLSTR-----IPQDKCNTLLTECDFS-SLSKYGDHLIRNAERADEHSDVNTTFC 106  
 QY 130 PERNRSTILTRPGMEIKKXGFHVLIEDLGPOFE-----FLVAYKRE 173  
 DB 107 PV--DPTIIGPPQMGVYVLADSL--HMRFLAPKIENEYETWTKMYNSMTYNQYM--K 160  
 QY 174 PGAEHAKYMRSGGIPRHLETMEPGAICYKAQTFVKAIGKYSASFOTECYE-VQGEAIP 232  
 DB 161 NGTDEKFKQITPQYDFEY-LNRLEPWTYCVQVQKFLPDRNKAQMSBPVEQYTHDETPV 219  
 QY 233 ---LVLLAFVGFMLILVVPVLF--VWKKGRLLQYSCCPVVPVLPYLK 276  
 DB 220 SMWAVVILMASV-FMVCLLALGCESLIMCYKTKKAFSPRNSLPOLK 267

## RESULT 2

INGS\_HUMAN STANDARD; PRT; 337 AA.

QY 01-OCT-1994 (Rel. 30, Created)  
 DT 01-OCT-1994 (Rel. 30, Last sequence update)  
 DE INTERFERON-GAMMA RECEPTOR BETA CHAIN PRECURSOR (INTERFERON-GAMMA RECEPTOR ACCESSORY FACTOR-1) (AF-1) (INTERFERON-GAMMA TRANSDUCER-1).  
 GN IFNGR2 OR IFNGR1.  
 OS Homo sapiens (human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 OX NCBI\_Taxid=9606;  
 RN 11  
 RP TISSUE FROM N.A.  
 RC TISSUE-Lung, fibroblast;  
 RX MEDLINE=94170380; PubMed=8124716;  
 RA Soh J., Donnelly R.J., Kotenko S., Mariano T.M., Cook J.R., Wang N., Emanuel S.L., Schwartz B., Miki T., Pestka S.;  
 RT Identification and sequence of an accessory factor required for activation of the human interferon gamma receptor.;  
 RL Cell 76:793-802(1994).  
 RN 12  
 RP SEQUENCE OF 1-24 FROM N.A.  
 RX MEDLINE=97067142; PubMed=8910544;  
 RA Rhee S., Ebensperger C., Dembic Z., Pestka S.;  
 RT The structure of the gene for the second chain of the human

FT Interferon gamma receptor.;  
 RL J. Biol. Chem. 271:28947-28952(1996).  
 CC -1- FUNCTION: PART OF THE RECEPTOR FOR INTERFERON GAMMA. REQUIRED FOR SIGNAL TRANSDUCTION. THIS ACCESSORY FACTOR IS AN INTEGRAL PART OF THE IFN-GAMMA SIGNAL TRANSDUCTION PATHWAY AND IS LIKELY TO INTERACT WITH GAF, JAK1, AND/OR JAK2.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC -----

CC EMBL: U05875; AAA16955.1; -;  
 DR EMBL: U05877; AAA16956.1; -;  
 DR EMBL: U68755; AAC52066.1; -;  
 DR MIM: 147569; -;  
 DR MIM: 209950; -;  
 DR InterPro: IPR001777; -;  
 DR Pfam: Pf00041; fn3; 1.  
 DR Receptor; Transmembrane; Glycoprotein; Signal; Repeat.  
 FT SIGNAL 1 27 POTENTIAL.  
 FT CHAIN 28 337 INTERFERON-GAMMA RECEPTOR BETA CHAIN.  
 FT DOMAIN 28 247 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 248 268 POTENTIAL.  
 FT DOMAIN 269 337 CYTOPLASMIC (POTENTIAL).  
 FT CARBOHYD 56 56 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 85 85 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 110 110 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 137 137 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 219 219 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 231 231 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT VARIANT 64 64 R -> Q.  
 FT VARIANT 64 64 R -> Q.  
 SO SEQUENCE 337 AA; 37834 MM; 18C61B10AD90E509 CRC64;

Query Match 11.0%; Score 178.5; DB 1; Length 337;  
 Best Local Similarity 26.1%; Pred. No. 1.1e-08;  
 Matches 75; Conservative 42; Mismatches 123; Indels 47; Gaps 14;

QY 11 WTSLEFMWFFALLPCULTDEVALIPAPONLSVSTNKKHLLMSPIYAPGET--VYYSV 68  
 DB 6 LMSLLILGVRAAAAAAPDPDLPOLAPQHPKIRLYNBOYLSMEPVALSNTSPVYTRV 65  
 QY 69 EYQGEYESLYTSHWIPSSWCSLTGEGPCDVDDITATVP-----YNLRATLGS 119  
 DB 66 QFKYTSQWFPADLMSIGVNCQTATFEC---DPTASPSAGFPMDPNVTLRLAEALGA 121  
 QY 120 QTSANSL---KHPPNRSTILTRPGMEIKKXGFHVL-----ELEDLGPOFE-FLVAY 169  
 DB 122 LHSAMVWTPMPEOH--YRNVTVGPPENIEVTPGEGSLIIRFSSPFDIADTSTAFPCYYHY 179  
 QY 170 WXPREGAEHNR-NVRSGGIPVHLETMEPGAICYKAQ-----TFKATIGYSAFSQT 221  
 DB 180 W--EKGGIQQYKGPFRNSI--SLDNLKPSRYCQVQAOQLMKNKSNIFRGHLSNIS-- 233  
 QY 222 ECVVEQGEA-IPVYLALPAFVGFMLILVVP---LFWKKGRLLQY 263  
 DB 234 -CYETMDASDELQVILISVGFSLSVIAGACFPYLUKRYGLIKY 279

## RESULT 3

INRL\_MOUSE STANDARD; PRT; 590 AA.

ID INRL\_MOUSE  
 AC P33896.  
 DT 01-FEB-1994 (Rel. 28, Created)  
 DT 01-FEB-1994 (Rel. 28, Last sequence update)



DE 30-MAY-2000 (Rel. 39, Last annotation update)  
DT INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).  
GN IFNARI OR IFNAR OR IFAR.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_Taxid=10090;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=92262522; PubMed=15393935;  
RA Uze G., Lutfalla G., Bandu M.T., Proudhon D., Mogensen K.E.;  
RT "Behavior of a cloned murine interferon alpha/beta receptor expressed  
in homospesific or heterospesific background";  
RL Proc. Natl. Acad. Sci. U.S.A. 89:4774-4778(1992).  
CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE  
CC I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS  
CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-  
CC SUBUNITS THEMSELVES.  
CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
CC -I- SIMILARITY: CONTAINS 2 FIBRINOCTIN TYPE III-LIKE DOMAINS.  
CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.

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EMBL; M89641; AAA37890.1; -.  
DR PIR; A45283; A45283.  
DR MGD; MG1:107658; Ifnar.  
KW Receptor; Transmembrane; Glycoprotein; Signal.  
FT SIGNAL 1 26  
FT CHAIN 27 590  
FT FT  
FT DOMAIN 27 429 EXTRACELLULAR (POTENTIAL).  
FT TRANSMEM 430 449 POTENTIAL.  
FT DOMAIN 450 590 CYTOPLASMIC (POTENTIAL).  
FT DISULFD 78 86 BY SIMILARITY.  
FT DISULFD 199 220 BY SIMILARITY.  
FT CARBOHYD 43 43 N-LINKED (GLCNAG. . .) (POTENTIAL).  
FT CARBOHYD 109 109 N-LINKED (GLCNAG. . .) (POTENTIAL).  
FT CARBOHYD 181 181 N-LINKED (GLCNAG. . .) (POTENTIAL).  
FT CARBOHYD 214 214 N-LINKED (GLCNAG. . .) (POTENTIAL).  
FT CARBOHYD 314 314 N-LINKED (GLCNAG. . .) (POTENTIAL).  
FT CARBOHYD 370 370 N-LINKED (GLCNAG. . .) (POTENTIAL).  
FT CARBOHYD 409 409 N-LINKED (GLCNAG. . .) (POTENTIAL).  
FT CARBOHYD 413 413 N-LINKED (GLCNAG. . .) (POTENTIAL).  
SEQUENCE 590 AA; 65776 MW; 7EC6DFE370185D3A CRC64;

```

      3 TPTAVLEELIMTSLFMPFYPALIPCLLTDEVALTPAPDNLSVLSMMKLHMSPIYAGE 62
      ::::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 197 TYCLEVKAIHSLLKXHSNTSYQCISTIVANKMPPGNLDYDAQGRSTYLKND-YIASAD 255
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 63 TVYYSVEVOGEYESLYTSHI-WISSWCSLNEGPECVDITDITATVPYNLNRATLGSQ 120
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 256 VLFRAQMLPGRSSSGSSGSKMKRPIPNCANVQTHCVFSDQTYVTGTGFHLVQASEGHN 315
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 121 TSAMSLKHPRFNRSIIITRGCMETAXKKGFHLVIEL---EDIGPFPEFLVAWKREPCAE 177
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 316 TSFWSEEFISQKHILPPPPIVITVAMSDDLTVLVNCDSDCDELINELIIFW--ENTSN 373
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

Oy 178 EHVKVVRSGGIDPVHLETPEPGAAYCVKAQTFVKA-IGXYSAVSQFECEYGVGEALPIVIA 236
      :|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db 374 TKISKEKDP-EFTLKLNQPLTVTCVQAVALFRALLAKTSTNSSEKLCEETRRGSGSTTWI 432

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Query Match 11.0%; Score 178.5; DB 1; Length 590;  
Best Local Similarity 23.0%; Pred. No. 2.1e-08;  
Matches 76; Conservative 63; Mismatches 163; Indels 29; Gaps 13;

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OY      237 LEAF-VGMLIVVPL-FVMKSGRLDYSCCPVVLLPDITLK---ITSRPOK---LISCR 289
          : |::|::| | FWMK | | Y S C P V V L L P D I T K | | : : : | | | : :
Db       433 ITGLGVFFSVAVLYALASVKM----YLCHVCPPPLAKPRRSIDFSEPSKNVLTLTAE 489
          : |::|::| | FWMK | | Y S C P V V L L P D I T K | | : : : | | | : :
OY      290 -----EEVDACATAYN-SPELLRAMIS 311
          : |::|::| | FWMK | | Y S C P V V L L P D I T K | | : : : | | | : :
Db       490 HTERCFIENMTDTVAVEVKAHPEEDLRKYSS 520
          : |::|::| | FWMK | | Y S C P V V L L P D I T K | | : : : | | | : :

RESULT   4
IIOS_MOUSE STANDARD:    PRt:     349 AA.
ID        IIOS_MOUSE
AC         061190:
DT         01-OCT-2000 (Rel. 4.0, Created)
DT         01-OCT-2000 (Rel. 4.0, Last sequence update)
DT         01-OCT-2000 (Rel. 4.0, Last annotation update)
DE         INTERLEUKIN-10 RECEPTOR BETA CHAIN PRECURSOR (IL-10R-B) (IL-10R2)
DE         (CYTOKINE RECEPTOR CLASS-II CRP2-4).
GN         IL10RB OR CRPB4.
OS         Mus musculus (Mouse).
OC         Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC         Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX         NCBI_TaxID=10090.
RN         [1]
RP         SEQUENCE FROM N.A.
RX         GIBBS.V.C., Pennica D.: Pubmed=9047351;
RA         "CRP2-4: Isolation of cDNA clones encoding the human and mouse proteins." ;
RT         Gene 186:97-101(1997).
RL         [2]
RM         CHARACTERIZATION.
RX         MEDLINE=98130620; Pubmed=9463407;
RA         Spencer S.D., Di Marco F., Hooley J., Pitts-Meek S., Bauer M.,
RT         Ryan A.M., Soradat B., Gibbs V.C., Aguet M.;
RT         "The orphan receptor CRP2-4 is an essential subunit of the interleukin 10 receptor ";
RL         J. Exp. Med. 187:571-578(1998).
CC         -I- FUNCTION: RECEPTOR FOR IL-10. SERVES AS AN ACCESSORY CHAIN ESSENTIAL FOR THE ACTIVE IL-10 RECEPTOR COMPLEX AND TO INITIATE IL-10-INDUCED SIGNAL TRANSDUCTION EVENTS.
CC         -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC         -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.
CC         -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC         -----
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CC         -----
CC         EMBL; U53696; AAC53062.1; -.
DR         MGd; MG1:109380; 11101D.
DR         InterPro; IPRO00282; -.
DR         InterPro; IPRO01777; -.
PF         Pfam; PF00041; fn3; 1.
KW         Receptor; Transmembrane; Glycoprotein; Signal.
FT         SIGNAL                     1..19              POTENTIAL.
FT         DOMAIN                     20..349           INTERLEUKIN-10 RECEPTOR BETA CHAIN.
FT         TRANSMEM                    220..220         EXTRACELLULAR (POTENTIAL).
FT         TRANSMEM                    242..241         CYTOPLASMIC (POTENTIAL).
FT         DOMAIN                      113..113          FIBONECTIN TYPE-III.
FT         DISULFID                     66..74            BY SIMILARITY.
FT         CARBOHYD                       49             BY SIMILARITY.
FT         CARBOHYD                      102             N-LINKED (GLCNAG. . ) (POTENTIAL).
FT         CARBOHYD                      161             N-LINKED (GLCNAG. . ) (POTENTIAL).
FT         CARBOHYD                      199             N-LINKED (GLCNAG. . ) (POTENTIAL).
SQ         SEQUENCE                   349 AA; 39774 MW; 5BBA4FB8B630A39 CRC64;

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Query Match          10.5%; Score 170.5; DB 1; Length 349;
Best Local Similarity 23.3%; Pred. No. 5.8e-08;
Matches 67; Conservative 47; Mismatches 120; Indels 53; Gaps 13;

QY 23 LIPC-----LLTDEVALIPAPDNLSVLTNNKHLMTMSPVIAFGETVYVSVEQGEY 74
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 1 MAPCVAGMLGGLFVLPAVGMIPPEKVMNSVNFKNILQWIEVPAEPKKNLFTMQYE-SY 59
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 75 ESLTSHMTSSSMCSLTGEPEDCVTDITATVPNLNRYATLSSQTSAM-SILKHPPNR 133
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 60 RS-PQDH-----CKRPASTQCDFS-HLSRYGDTYVRVRLADEHSEMNVAVFECPV-- 108
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 134 NSTLFRGMEIIXKXGFLVLELDIGQFE-----FLVYKMKRPGAE 177
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 109 EDTIIGPEPMQIESAEEL--HLRSPAQIENEPETWTLKNIYDSMAYRVOYW--KNGTN 164
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 178 EHVKNVRSGGIPVHLETPMEPGAVCYKQAQTFVKAIGXSAESQTECVVEQGE----- 229
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
   165 EKQVGVSPYDSEV-LRNLEPWTTCYCIQVGFLLDQNPRTGEMSEPICERTGNDETPSMIV 223
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

QY 230 AIPVLALFAVGFNLLIVVPLPFWKKGRLQYSCCVVLVPLDTLK 276
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
Db 224 AIIIVSVLVVFLFLGCEV--LMIILYKTKTHTFSGTSLPDLK 267
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 5
INRL_BOVIN STANDARD; PRT; 560 AA.
AC 004790;
DT 01-OCT-1993 (Rel. 27, Created)
DT 01-FEB-1994 (Rel. 28, Last sequence update)
DT 01-NOV-1997 (Rel. 35, Last annotation update)
DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC).
GN IFNARI OR IFNAR.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=93076908; PubMed=1446745;
RA Mouchel-Vielh E., Lutfalla G., Mogensen K.E., Uze G.;
RT "Specific antiviral activities of the human alpha interferons are
RT determined at the level of receptor (IFNAR) structure.";
RT FEBS Lett. 313:255-259(1992).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=Lung;
RX MEDLINE=93305725; PubMed=6318540;
RA Lam J.-K., Langer J.A.;
RT "Cloning and characterization of a bovine alpha interferon receptor.";
RL Blochm. Biophys. Acta 1173:314-319(1993).
RT -1- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE
RT I IFNS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS
RT INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-
RT SUBUNTS THEMSELVES.
CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.
CC -1- SIMILARITY: CONTAINS 2 FIBROBLAST TYPE III-LIKE DOMAINS.
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.
CC
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CC or send an email to license@sib-sib.ch).
CC
OR EMBL; X68443; CAA48484.1; -
OR EMBL; L06320; AAA02571.1; -
OR PIR; S33770; S33770.
OR

```

|            |   |                  |                                     |
|------------|---|------------------|-------------------------------------|
| DR         | PfR:  | S27387;          | S27387.                             |
| DR         | InterPro:   | IPR001777.       | -                                   |
| DR         | Pfam:   | PF000041:        | fnc3_1.                             |
| KM         | Receptor:   | Transmembrane:   | Glycoprotein; Signal.               |
| FT         | SIGNAL  | 1                | 24                                  |
| FT         | CHAIN   | 25               | 560                                 |
| FT         | DNAIN   | 25               | 437                                 |
| FT         | TRANSEM   | 438              | 458                                 |
| FT         | DNAIN   | 459              | 560                                 |
| FT         | DISULFID  | 76               | 84                                  |
| FT         | DISULFID  | 199              | 220                                 |
| FT         | CARBOHYD  | 47               | 47                                  |
| FT         | CARBOHYD  | 55               | 55                                  |
| FT         | CARBOHYD  | 85               | 85                                  |
| FT         | CARBOHYD  | 109              | 109                                 |
| FT         | CARBOHYD  | 172              | 172                                 |
| FT         | CARBOHYD  | 254              | 254                                 |
| FT         | CARBOHYD  | 313              | 313                                 |
| FT         | CARBOHYD  | 377              | 377                                 |
| FT         | CARBOHYD  | 434              | 434                                 |
| FT         | CONFLICT  | 422              | 422                                 |
| SQ         | SEQUENCE  | 560 AA;          | 63818 MW; 66D76B72861E1D11 CMC64;   |
| OY         | Query Match   | 10.1%;           | Score 164.5; DB 1; Length 560;      |
|            | Best Local Similarity   | 21.9%;           | Pred. No. 3.5e-07;                  |
|            | Matches 70;   | Conservative 62; | Mismatches 136; Indels 51; Gaps 14; |
| OY         | 21 YALIFCLLTDEVALIPAPONLSYLSTNNKHLHLMSPVLAPEGTYVYSVEYGGEYSILTS        | 80               |                                     |
| DB         | 215 YSPVICINTTEKHKPSPENDIQINDNOIYLVK-----DYENMTFPQAWLRAPFK            | 267              |                                     |
| OY         | 81 HI-----W-ISSPSCSLTEGPECDDTDDTTATVPYNLIRVALIGSOTASWLTKHPF           | 131              |                                     |
| DB         | 268 KIPGHSDSKMQIPIR--CENWTSTHCVPREKVSNGITYYVARAANGSGTSPWESEKEFN       | 325              |                                     |
| OY         | 132 NRNSTILLRRPGM---EIKKXGFHLVI----LEEDIGPO----FEELVAYVAREPAEHY       | 180              |                                     |
| DB         | 326 TEMKTIIIPPVLISVKSVDSDLSHVSAGASESENNSVOLPLILEVIVEMENTSNAEKRV       | 385              |                                     |
| OY         | 181 KMVRSGGIPIVHLETMEPGAACVKRAKOTEVK--AIQXSASFOSQECVEVO---GEAIPLV     | 234              |                                     |
| DB         | 386 LEKRINFIL---PPDLKPLTVICVKARALIENDRRKKGSSFDSPTVECKTRPGNTSTWLIY     | 442              |                                     |
| OY         | 235 LALFAVFEMLLLVVPLFLFWMKGRLLQYSCCPVVVLPDPTK--ITSNPK--LISCREE        | 290              |                                     |
| DB         | 443 GTCTALFSIPVIVVSVFL---RCVKYVFPPSSKPPSSVDEYSDPDRLRLTLSTSEE          | 498              |                                     |
| OY         | 291 EYDAC-----ATAVMSPRE   | 304              |                                     |
| DB         | 499 QTERCFIIEMASTITEIBE   | 517              |                                     |
| INRL_HUMAN | 6   |                  |                                     |
| ID         | INRL_HUMAN  | STANDARD:        | PRT: 557 AA.                        |
| AC         | PI181;  |                  |                                     |
| DT         | 01-AUG-1990 (Rel. 15, Created)  |                  |                                     |
| DT         | 01-AUG-1990 (Rel. 15, Last sequence update)                           |                  |                                     |
| DT         | 01-OCT-2000 (Rel. 40, Last annotation update)                         |                  |                                     |
| DE         | INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC). |                  |                                     |
| GN         | IFNA1 OR IFNA1N.  |                  |                                     |
| OS         | Homo sapiens (Human).   |                  |                                     |
| OC         | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;     |                  |                                     |
| OC         | Mammalia; Euteria; Primates; Carnivora; Homiidae; Homo.               |                  |                                     |
| OX         | NCBI_Taxid=9606;  |                  |                                     |
| RN         | [1]   |                  |                                     |
| RP         | SEQUENCE FROM N.A.  |                  |                                     |
| RX         | MEDLINE=90124632; PubMed=2153461;                                     |                  |                                     |
| RA         | Uze G., Iutalia G., Gresser I.;                                       |                  |                                     |
| RT         | "Genetic transfer of a functional human interferon alpha receptor     |                  |                                     |
| RT         | into mouse cells: cloning and expression of its cDNA."                |                  |                                     |

RL Cell 60:225-234(1990).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RA MEDLINE-92129376; PubMed-1370833;  
 RA Lutfalla G., Gardner K., Proudhon D., Vielh E., Uze G.;  
 RT "The structure of the human interferon alpha/beta receptor gene.";  
 RL J. Biol. Chem. 267:2802-2809(1992).  
 RN [3]  
 RP PHOSPHORYLATION BY TYK2.  
 RA MEDLINE-95059042; PubMed-7526154;  
 RA Colamonic O., Yan H., Domanski P., Handa R., Smalley D.,  
 RA Mullerman J., Witte M., Krishnan K., Krolewski J.;  
 RT "Direct binding to and tyrosine phosphorylation of the alpha subunit  
 of the type I interferon receptor by p135tyk2 tyrosine kinase.";  
 RL Mol. Cell. Biol. 14:8133-8142(1994).  
 CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE  
 CC I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS  
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-  
 CC SUBUNITS THEMSELVES.  
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -I- TISSUE SPECIFICITY: IFN RECEPTORS ARE PRESENT IN ALL TISSUES AND  
 CC EVEN ON THE SURFACE OF MOST IFN-RESISTANT CELLS.  
 CC -I- PTM: PHOSPHORYLATED ON TYROSINE RESIDUES BY TYK2 TYROSINE KINASE.  
 CC -I- SIMILARITY: CONTAINS 2 FIBRONECTIN TYPE III-LIKE DOMAINS.  
 CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
 CC -----  
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 CC or send an email to [license@sib-sib.ch](mailto:license@sib-sib.ch)).  
 CC -----  
 DR EMBL: J03171; AAA52730.1; -  
 DR EMBL: X60459; CAA42992.1; -  
 DR PIR: A32694; A32694.  
 DR PIR: S17112; S17112.  
 DR MIM: 107450; -  
 KM Receptor; Transmembrane; Glycoprotein; Signal; Polymorphism;  
 KM Phosphorylation.  
 FT SIGNAL 1 27  
 FT CHAIN 28 557  
 FT INTERFERON-ALPHA/BETA RECEPTOR ALPHA  
 FT CHAIN.  
 FT DOMAIN 28 436  
 FT TRANSMEM 437 457  
 FT DOMAIN 458 557  
 FT DISULFID 79 87  
 FT DISULFID 199 220  
 FT MOD\_RES 466 466  
 FT MOD\_RES 481 481  
 FT CARBOHYD 50 50  
 FT CARBOHYD 58 58  
 FT CARBOHYD 81 81  
 FT CARBOHYD 88 88  
 FT CARBOHYD 110 110  
 FT CARBOHYD 172 172  
 FT CARBOHYD 254 254  
 FT CARBOHYD 313 313  
 FT CARBOHYD 314 314  
 FT CARBOHYD 376 376  
 FT CARBOHYD 416 416  
 FT CARBOHYD 433 433  
 FT VARIANT 168 168  
 FT L -> V.  
 FT /FTID-VAR 002717.  
 FT CONFLICT 17 17 G -> A (IN REF. 2)  
 FT SEQUENCE 557 AA: 63525 MM: 06744C8A1ADEB73 CRC64;

Query Match 10.0%; Score 162.5; DB 1; Length 557;  
 Best Local Similarity 22.0%; Pred. No. 5.2e-07;  
 Matches 71; Conservative 54; Mismatches 115; Indels 83; Gaps 17;

QY 21 YALPCLTDEVALIPAPQNLSTYLNKHLMSPVLABETVYYSVEQGEYSLYT- 79  
 Db 215 YSPVCHIKTVEENELPPEENIEVSQNONVYWKW-----DYTYANNTPQVOMLHAFLK 267  
 QY 80 ----SHIWIPESWCSLFGPECDDTDDITATVPYN-----LRVATLSQTSAMS-- 125  
 Db 268 RNPQNHLY--KMQOI--PDCENKTKTQCVFPQVNFQKGIYLLKQVSDGNSVFSWEE 321  
 QY 126 -----ILKHPFNNSITLTPRGMEXKXGFHLV-----ELEDLGPQEF 165  
 Db 322 IKPDTIQAFLLPVPFNRS-----LSDSPHIITGAPKQSGNPVIQDYLYIE- 370  
 QY 166 LVATWKEPGEAEYKAVKRSQCIYVHLETPGAAVCYKAO--TFVKAIGXSAFSQTEC 223  
 Db 371 -IIFWENTSNAERKTIIEKT--DVTVPNLKPLTVYCYKARAHMDEKLNSSVFSDAVC 426  
 QY 224 VEVO-GEAIPVLVLAFAVGFMLIVYVPLVWMMGRLLQVSCPPVVLPTLKTNS-- 280  
 Db 427 EKTRPGNTSKTWL-----IVGICIALFALPFIYIAKAYFLR--CLNYVFPF-SLKPSISID 479  
 QY 281 -----PQK--LISCRREVDAC 295  
 Db 480 EYFSEQPLKNLLSTSEQIEKC 502  
 RESULT 7  
 INRL SHEEP STANDARD; PRT; 560 AA.  
 ID 028589: 095206;  
 AC 01-NOV-1997 (Rel. 35, Created)  
 DT 01-NOV-1997 (Rel. 35, Last sequence update)  
 DT 30-MAY-2000 (Rel. 39, Last annotation update)  
 DE INTERFERON-ALPHA/BETA RECEPTOR ALPHA CHAIN PRECURSOR (IFN-ALPHA-REC)  
 DE (INTERFERON-ALPHA/BETA RECEPTOR-1).  
 GN IFNARI OR IFNAR.  
 OS Ovis aries (Sheep).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Caprinae; Ovis.  
 OX NCBI\_Taxid=9940;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Endometrium;  
 RX MEDLINE-97135690; PubMed-8981227;  
 RA Kaluz S., Fisher P.A., Kaluzova M., Sheldrick E.L., Flint A.P.F.;  
 RT "Structure of an ovine interferon receptor and its expression in  
 RT endometrium.";  
 RL J. Mol. Endocrinol. 17:207-215(1996).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Endometrium;  
 RX MEDLINE-98006426; PubMed-9348203;  
 RA Han C.-S., Mathialagan N., Klemann S.W., Roberts R.M.;  
 RT "Molecular cloning of ovine and bovine type I interferon receptor  
 RT subunits from uteri, and endometrial expression of messenger  
 RT ribonucleic acid for ovine receptors during the estrous cycle and  
 RT pregnancy.";  
 RL Endocrinology 138:4757-4767(1997).  
 CC -I- FUNCTION: RECEPTOR FOR INTERFERONS ALPHA AND BETA. BINDING TO TYPE  
 CC I FENS TRIGGERS TYROSINE PHOSPHORYLATION OF A NUMBER OF PROTEINS  
 CC INCLUDING JAKS, TYK2, STAT PROTEINS AND IFN-R ALPHA-AND BETA-  
 CC SUBUNITS THEMSELVES.  
 CC -I- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -I- TISSUE SPECIFICITY: EXPRESSED IN ALL TISSUES EXAMINED EXCEPT  
 CC CONCEPTUS AT DAY 15 OF PREGNANCY.  
 CC -I- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
 CC -----  
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|    |  |
|----|--|
| CC | Mammalia;Eutheria: Primates; Catarrhini; Hominoidea; Homo.   |
| OX | NCBI_TaxID=9606;   |
| RN | [1]  |
| RP | SEQUENCE FROM N.A.   |
| RC | TISSUE=Lymphoma;   |
| RX | MEDLINE=94165477; PubMed=8120391;  |
| RA | Liu Y., Wei S.H.-Y., Ho A.S.-Y., de Waal Malefyt R., Moore K.W.;   |
| RT | *Expression cloning and characterization of a human IL-10 receptor.;   |
| RL | J. Immunol. 152:1821-1829(1994).   |
| CC | -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.  |
| CC | -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.   |
| CC | -1- TISSUE SPECIFICITY: SPLEEN, THYMUS, AND PANC. FAINT EXPRESSION   |
| CC | IN PANCREAS, SKELETAL MUSCLE, BRAIN, HEART, AND KIDNEY. PLACENTA,  |
| CC | LUNG, AND LIVER SHOWED INTERMEDIATE LEVELS. MONOCYTES, B CELLS,  |
| CC | LARGE GRANULAR LYMPHOCYTES, AND T CELLS EXPRES HIGH LEVELS OF IL-  |
| CC | 10R.   |
| CC | -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  |
| CC |  |
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| CC | or send an email to <a href="mailto:license@isb-sib.ch">license@isb-sib.ch</a> ).  |
| CC |  |
| DR | EMBL: U00672; AAA17896.1; .  |
| DR | MTM: 146933; .   |
| KM | Receptor; Transmembrane; Glycoprotein; Signal.   |
| FT | SIGNAL   |
| FT | 1 21   |
| FT | CHAIN 22 578   |
| FT | POTENTIAL.   |
| FT | INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.   |

|          |                       |   |                 |                    |                                     |
|----------|-----------------------|---|-----------------|--------------------|-------------------------------------|
|          | FT                    | DOMAIN  | 257             | 578                | CYTOPLASMIC (POTENTIAL).            |
|          | FT                    | DISELTD   | 202             | 223                | POTENTIAL.                          |
|          | FT                    | CARBOHYD  | 50              | 50                 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
|          | FT                    | CARBOHYD  | 74              | 74                 | N-LINKED (GLCNAC. . .) (POTENTIAL). |
|          | FT                    | CARBOHYD  | 110             | 110                | N-LINKED (GLCNAC. . .) (POTENTIAL). |
|          | FT                    | CARBOHYD  | 154             | 154                | N-LINKED (GLCNAC. . .) (POTENTIAL). |
|          | FT                    | CARBOHYD  | 177             | 177                | N-LINKED (GLCNAC. . .) (POTENTIAL). |
|          | FT                    | CARBOHYD  | 189             | 189                | N-LINKED (GLCNAC. . .) (POTENTIAL). |
|          | SQ                    | SEQUENCE  | 578 AA;         | 62903 MW;          | EELB29064338157C CRC64;             |
|          | Query Match           |   | 8.4%            | Score 136:         | DR 1; Length 578;                   |
|          | Best Local Similarity |   | 23.8%;          | Pred. No. 0.00012; |                                     |
|          | Matches 70;           | Conservative 47;  | Mismatches 109; | Indels 68;         | Gaps 14;                            |
| Oy       | 23                    | LIPCLLPDEVAI-----LLAPONLSVSTMMKHLMLMSPVIAPEGFYYSVE            | 69              |                    |                                     |
|          | :::: :: :             | : :: :: :   | : : :~ :        | :                  |                                     |
| Dd       | 1                     | MIPCILLALLLSLRGSDAHGTLPBPSPSWFAEFFFHILHTPTLPNOSSESCYEYA       | 60              |                    |                                     |
| Oy       | 70                    | YOGEYESLYTSHIWIPSSWCSLTTEGPED-VDDITATVPYNLRVRATIGSOTSAMSILK   | 128             |                    |                                     |
|          |                       |   |                 |                    | :                                   |
| Dd       | 61                    | L-----LATGIESMNSINSCOTLSYDLTAVTLDLHSNGRRARRAADA GSRHSNWITYTN  | 115             |                    |                                     |
| Oy       | 129                   | HPPNNNSTILT-RPGMEIKKKXGFHL-VIEL-----EDLGQOF-EFLVAYMYXR        | 172             |                    |                                     |
|          | ::  ::                | ::  ::  | ::  ::          | ::  ::             | :                                   |
| Dd       | 116                   | TRESVDEVTLTVGVSNLEIH-N-GRITLKIQLPKPMADANDTYESI-FSHFREYETAI-RK | 173             |                    |                                     |
| Oy       | 173                   | EPG-----AEHVAKMNRSGGIPIVULEMTPEPCAAVCYKAQTIVKALGXIASAFSOTEC   | 223             |                    |                                     |
|          | :                     | :: :  | :: :            | :: :               | :                                   |
| Dd       | 174                   | VPGNETFTHKKVKKHENFSLTSGEV-----GEFCVOYKPSPVASRSMNGMSKECC       | 223             |                    |                                     |
| Oy       | 224                   | VEV--OGCAIFPLVLALPAFV---GFMLLVVVPLFWFKMGRLGYSCCPVVYL          | 271             |                    |                                     |
|          | ::  ::                | ::  ::  | ::  ::          | ::  ::             | ::  ::                              |
| Dd       | 224                   | ISLTRQTFYTVNVNIIEFAFVLLSGALNYCALQLIVYRRKKL-----PSVLL          | 271             |                    |                                     |
| RESULT   | 9                     |   |                 |                    |                                     |
| TF_RABIT |                       | STANDARD:   | PRT:            | 292 AA.            |                                     |
| ID       | TF_RABIT              |   |                 |                    |                                     |
| NC       | P24055;               |   |                 |                    |                                     |

DT 01-MAR-1992 (Rel. 21, Created)  
 DT 01-MAR-1992 (Rel. 21, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).  
 GN F3.  
 OS Oryctolagus cuniculus (Rabbit).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.  
 OX NCBI\_TaxID=9986;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Heart;  
 RX MEDLINE=91200676; PubMed=1840552;  
 RA Andrews B.S., Rehenculla A., Fowler B.J., Edgington T.S., Mackman N.;  
 RT "Conservation of tissue factor primary sequence among three mammalian  
 species.";  
 RL Gene 98:265-269(1991).  
 RN [2]  
 RP SEQUENCE OF 33-292 FROM N.A.  
 RC STRAIN=NEW ZEALAND WHITE; TISSUE=Brain;  
 RX MEDLINE=92081032; PubMed=1746002;  
 RA Pasvashe A., Ezekowitz M., Lin T.C., Horton R., Bach R., Konigsberg W.;  
 RT "Molecular cloning, characterization and expression of cDNA for  
 rabbit brain tissue factor.";  
 RL Thromb. Haemost. 66:315-320(1991).  
 RN [3]  
 RP X-RAY CRYSTALLOGRAPHY (2.35 ANGSTROMS) OF 36-240.  
 RX MEDLINE=98266351; PubMed=9605315;  
 RA Muller Y.A., Kelley R.F., de Vos A.M.;  
 RT "Hinge bending within the cytokine receptor superfamily revealed by  
 the 2.4 A crystal structure of the extracellular domain of rabbit  
 tissue factor.";  
 RL Protein Sci. 7:1106-1115(1998).  
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES  
 FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN  
 NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 PROPAagation OF THE COAGULATION PROTEASE CASCADE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- TISSUE SPECIFICITY: BRAIN, HEART.  
 CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.  
 CC -----  
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 or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC -----  
 DR EMBL; M55390; AAA63469.1; -;  
 DR EMBL; X53521; -; NOT\_ANNOTATED\_CDS.  
 DR PIR; J00441; KFRB3.  
 DR PIR; S23681; S23681.  
 DR PIR; IA21; 27-MAY-98.  
 DR InterPro; IPR001187; -;  
 DR Pfam; PF01108; Tissue\_fac; 1.  
 DR PRINTS; PRO0346; TISSUEFACTOR.  
 DR PROSITE; PS00621; TISSUE\_FACTOR; 1.  
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
 KW Palmitate; 3D-structure.  
 FT CHAIN 1 32  
 FT SIGNAL 1 32  
 FT CHAIN 33 292  
 FT DOMAIN 33 250  
 FT TRASNEM 251 271  
 FT DOMAIN 272 292  
 FT SITE 44 46  
 FT SITE 75 77  
 FT CARBOHYD 41 41  
 FT CARBOHYD 114 114  
 FT CARBOHYD 154 154  
 FT CARBOHYD 167 167  
 FT CARBOHYD 182 182  
 TISSUE FACTOR.  
 EXTRACELLULAR (POTENTIAL).  
 POTENTIAL.  
 CYTOPLASMIC (POTENTIAL).  
 WKS MOTIF.  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 N-LINKED (GLCNAC. . .) (POTENTIAL).

FT DISULFID 79 87  
 FT DISULFID 216 239  
 FT LIPID 274 274  
 SQ SEQUENCE 292 AA; 32738 MW; 4860A1CDBACFF71 CRC64;  
 Query Match 8.0%; Score 130; DB 1; Length 292;  
 Best Local Similarity 24.0%; Pred. No. 0.00019;  
 Matches 61; Conservative 34; Mismatches 101; Indels 58; Gaps 11;  
 QY 40 NLVLSTNNKHLMMSPVIAAGETVYVSYVQGESELYSHI-----WIPSSMCSTLE 93  
 DB 41 NLVSTNNKFTLEWEP-----KSIDH-----VYVOISTRLENN--KSCFELTA 83  
 QY 94 GPCEDVDDITATV--PYNLVRATLGSQTSAMSILKHPFRNS-----TLITPRGM 143  
 DB 84 ETECDLDEYVKDVGQYMARVLSYPARNQNTGTFPEEPFRNSPEFTPYLDTNLGQPTI 143  
 QY 144 E-IXKGFHLVLEED-----LGPFELVAYWXPBGAEHVKWRS 185  
 DB 144 QSEQVGTKLNTVQDARTLVRRNGTFLSLRAVGRKDLNTLYYWR-----ASTGKKVAT 199  
 QY 186 GGIPVHLTEHPGAAYVKAQTFV--KAIGKYSFSTGEV--EVQGAIPLYALPAFVG 242  
 DB 200 TTNTEFLIDYDKGENYCFVQAVIPSRKRORSPESLTECTSRQGRAREMFFIGAVV 259  
 QY 243 FMLIVVPLFVWK 256  
 DB 260 VALLIIVSTVYK 273  
 RESULT 10  
 TF\_HUMAN  
 ID TF\_HUMAN STANDARD; PRT; 295 AA.  
 AC P13726;  
 DT 01-JAN-1990 (Rel. 13, Created)  
 DT 01-JAN-1990 (Rel. 13, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III)  
 DE (THROMBOPLASTIN) (CD142 ANTIGEN).  
 GN F3.  
 OS Homo sapiens (Human).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 OX NCBI\_TaxID=9606;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=89247359; PubMed=2719931;  
 RA Mackman N., Morrissey J.H., Fowler B., Edgington T.S.;  
 RT "Complete sequence of the human tissue factor gene, a highly  
 regulated cellular receptor that initiates the coagulation protease  
 cascade.";  
 RT RT cascade.";  
 RL Biochemistry 28:1755-1762(1989).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87260946; PubMed=3037536;  
 RA Spicer E.K., Horton R., Bloem L., Bach R., Williams K.R., Guha A.,  
 Kraus J., Lin T.C., Nemerson Y., Konigsberg W.H.;  
 RT "Isolation of cDNA clones coding for human tissue factor: primary  
 structure of the protein and cDNA.";  
 RT Proc. Natl. Acad. Sci. U.S.A. 84:5148-5152(1987).  
 RN [3]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=87244317; PubMed=3297348;  
 RA Morrissey J.H., Fakhrat H., Edgington T.S.;  
 RT "Molecular cloning of the cDNA for tissue factor, the cellular  
 receptor for the initiation of the coagulation protease cascade.";  
 RT Cell 50:129-135(1987).  
 RN [4]  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE=88050796; PubMed=2823875;  
 RA Scarpati E.M., Wen D., Broze G.J. Jr., Miletich J.P.,  
 Flanderer R.R., Siegel N.R., Sadler J.E.;

RT Human tissue factor: cDNA sequence and chromosome localization of  
 the gene." ;  
 RL Biochemistry 26:5234-5238(1987).  
 RN (5)  
 RP SEQUENCE FROM N.A.  
 RX MEDLINE-88100453; PubMed-3424286;  
 RA Fisher K.L., Gorman C.M., Vemar G.A., O'Brien D.P., Lavin R.M.;  
 RT "Cloning and expression of human tissue factor cDNA." ;  
 RL Thromb. Res. 48:89-99(1987).  
 RN (6)  
 RP DISULFIDE BONDS, AND PALMITOYLATION.  
 RX MEDLINE-89000604; PubMed-3166978;  
 RA Bach R., Konigsberg W.H., Nemerson Y.;  
 RT "Human tissue factor contains thioester-linked palmitate and stearate  
 on the cytoplasmic half-cysteine." ;  
 RL Biochemistry 27:4227-4231(1988).  
 RN (7)  
 RP X-RAY CRYSTALLOGRAPHY (3.0 ANGSTROMS) OF 33-243.  
 RX MEDLINE-94368785; PubMed-8086403;  
 RA Muller Y.A., Ullsch M.H., Kelley R.F., de Vos A.M.;  
 RT "Structure of the extracellular domain of human tissue factor:  
 location of the factor VIIa binding site." ;  
 RL Biochemistry 33:10864-10870(1994).  
 RN (8)  
 RP X-RAY CRYSTALLOGRAPHY (1.7 ANGSTROMS) OF 33-243.  
 RX MEDLINE-96190957; PubMed-8609606;  
 RA Muller Y.A., Ullsch M.H., de Vos A.M.;  
 RT "The crystal structure of the extracellular domain of human tissue  
 factor refined to 1.7-A resolution." ;  
 RL J. Mol. Biol. 256:144-159(1996).  
 RN (9)  
 RP X-RAY CRYSTALLOGRAPHY (2.0 ANGSTROMS) OF 33-251 IN COMPLEX WITH FVIIA.  
 RX MEDLINE-96175641; PubMed-8598903;  
 RA Banner D.M., D'Arcy A., Chene C., Winkler F.K., Guha A.;  
 RT "Konigsberg W.H., Nemerson Y., Kirchhofer D.;  
 RT "The crystal structure of the complex of blood coagulation factor  
 VIIa with soluble tissue factor." ;  
 RL Nature 380:41-46(1996).  
 RN (10)  
 RP X-RAY CRYSTALLOGRAPHY (2.1 ANGSTROMS) OF 37-242 IN COMPLEX WITH FVIIA.  
 RX MEDLINE-99126538; PubMed-9925787;  
 RA Zhang E., St Charles R., Tulinsky A.;  
 RT "Structure of extracellular tissue factor complexed with factor VIIa  
 inhibited with a BPTI mutant." ;  
 RL J. Mol. Biol. 285:2089-2104(1999).  
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES  
 FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN  
 NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- INDICATION: TF EXPRESSION IS HIGHLY DEPENDENT UPON CELL TYPE. TF  
 CAN ALSO BE INDUCED BY THE INFLAMMATORY MEDIATORS INTERLEUKIN 1  
 AND TNF. AS WELL AS BY ENDOTOXIN, TO APPEAR ON MONOCYTES AND  
 VASCULAR ENDOTHELIAL CELLS AS A COMPONENT OF CELLULAR IMMUNE  
 RESPONSE.  
 CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.  
 CC -1- DATABASE: NAME-PROT; NOTE-CD guide CD142 entry;  
 WWW-"http://www.ncbi.nlm.nih.gov/protow/CD/CD142.htm".  
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 or send an email to license@isb-sib.ch).  
 CC EMBL: J02931; AAA61150.1; -  
 DR EMBL: M16553; AAA61151.1; -  
 DR EMBL: J02846; AAA61152.1; -  
 DR EMBL: M27436; AAA61734.1; -  
 DR EMBL: A19048; CAA01438.1; -

DR PIR: A28320; KFH03.  
 DR PIR: A43645; A43645.  
 DR PIR: A47574; A47574.  
 DR PDB: 1BOY; 10-JUN-96.  
 DR PDB: 2HPT; 29-JAN-96.  
 DR PDB: 1DAN; 04-SEP-97.  
 DR PDB: 1AHW; 19-AUG-98.  
 DR PDB: 1TFH; 19-AUG-98.  
 DR PDB: 1FAK; 03-DEC-99.  
 DR MIM: 134390; -  
 DR InterPro: IPR001187; -  
 DR Pfam: PF01108; Tissue\_fac; 1.  
 DR PRINTS: PR00346; TISSUEFACTOR.  
 DR PROSITE: PS00621; TISSUE\_FACTOR; 1.  
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
 KW Palmitate; 3d-structure.  
 FT SIGNAL 1 32  
 FT CHAIN 33 295  
 FT DOMAIN 33 251  
 FT TRANSMEM 252 274  
 FT DOMAIN 275 295  
 FT SITE 46 48  
 FT SITE 77 79  
 FT SITE 190 192  
 FT CARBOHYD 156 156  
 FT CARBOHYD 169 169  
 FT DISULFID 81 89  
 FT DISULFID 218 241  
 FT LIPID 277 277  
 FT CONFLICT 260 260  
 FT SEQUENCE 295 AA; 33067 MW; D3486C71ED8BAD0 CRC64;  
 Query Match 7.7%; Score 125.5; DB 1; Length 295;  
 Best Local Similarity 23.4%; Pred. No. 0.00049;  
 Matches 63; Conservative 35; Mismatches 122; Indels 49; Gaps 12;

QY 13 TSLFMFEYALIPCLLTDEVALPAPONLSVLTNNKHLMSPYIAPGEVYYSVYOG 72  
 DB 19 TLLGWFVAQVAGAGSTNTV--AAYNLTWKSNTKLTLEMEP--KPVNOY-YTVQIST 72  
 QY 73 EYESLYTHIMIPSSWCSLTSPCEDVDITATV--PNNLVKATLGSOTSAWSLAKRP 130  
 DB 73 K-----SGDW--KSKCFYTTDTECDLDEIVKQVYIARVFSYPAGNVSTGSAGRP 124  
 QY 131 FNRRS-----TLTTRGME-IXKXGFHLYLEED-----LGPPE 164  
 DB 125 LYENSPETPYLETNIGOPTIOSFEQVGTKNVYVEDENTLYVRNNTPLSLDVFCKDLI 184  
 QY 165 FLVAYMXREPGEAEHVKNVRSGGIPVHLETPGAAVCYKAQTFV--KAIGYSAFSQTE 222  
 DB 185 YLYLVYWKSSSSSKTKAKT-----NTNPEFLDVQKGENYCSQVAVISRVNKRSTDSPE 240  
 QY 223 CV-EYQGEAIPLYVALFAVFGMLILVYV 250  
 DB 241 CMGQKGEFERELFYIIGAVVEVILVYI 269  
 RESULT 11  
 ID 110R\_MOUSE STANDARD: PRT; 575 AA.  
 AC 061727;  
 DT 15-JUL-1998 (Rel. 36, Created)  
 DT 15-JUL-1998 (Rel. 36, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE INTERLEUKIN-10 RECEPTOR ALPHA CHAIN PRECURSOR (IL-10R-A) (IL-10R1).  
 GN IL10RA OR IL10R.  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 CC Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.  
 CX NCBL\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.

RC STRAIN-C57BL/6 X AJ FL; TISSUE-Hematopoietic;  
 RA MEDLINE=9406585; PubMed=8248239;  
 RX Ho A.S.-Y., Liu Y., Khan T.A., Suhr D.-H., Bazan J.F., Moore K.W.;  
 RT "A receptor for interleukin 10 is related to interferon receptors."  
 RL Proc. Natl. Acad. Sci. U.S.A. 90:11267-11271(1993).  
 CC -1- FUNCTION: RECEPTOR FOR IL-10; BINDS IL-10 WITH A HIGH AFFINITY.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 DR EMBL; L12120; AAA16156.1; -  
 DR MGI; MGI:96338; 1110ra.  
 KW Receptor; Transmembrane; Glycoprotein; Signal.  
 FT SIGNAL 1 16  
 FT CHAIN 17 575 INTERLEUKIN-10 RECEPTOR ALPHA CHAIN.  
 FT DOMAIN 17 241 EXTRACELLULAR (POTENTIAL).  
 FT TRANSMEM 242 262 POTENTIAL.  
 FT DOMAIN 263 575 CYTOPLASMIC (POTENTIAL).  
 FT DISULFID 204 225 POTENTIAL.  
 FT CARBOHYD 50 50 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 66 66 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 113 113 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 182 182 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 FT CARBOHYD 238 238 N-LINKED (GLCNAC. . .) (POTENTIAL).  
 SQ SEQUENCE 575 AA; 64248 MW; 820B9CD576F686B7 CRC64;

Query Match 7.7%; Score 125.5; DB 1; Length 575;  
 Best Local Similarity 20.4%; Pred. No. 0.0011;  
 Matches 64; Conservative 53; Mismatches 121; Indels 75; Gaps 12;

QY 23 LIPCLLT-----DEVAL--LPAPONSVLSTNMKHLMSPVLAAGEVYYSVYQGE 73  
 DB 5 LIPCLLT-----DEVAL--LPAPONSVLSTNMKHLMSPVLAAGEVYYSVYQGE 73  
 QY 74 YESLYTSIWIPISSWCSLTGEPEDVT---DDITATVYPLNVRATLSSQTSAMSILKH 129  
 DB 63 ---QVGNSTWMDIHICRAQAALSCDLTFPTLDLHRSYVYRARRAVNDQSYSNMTTTER 119  
 QY 130 PPNRNSLTIT-----RPGMEIKKXGFHLVIELEDLPQEFELVAVYK 171  
 DB 120 RFTVDEVILTVDSVTLKAMDGIITGTHPRPTIPAGDEYQVEKDL-RVYKISIRKFS 178  
 QY 172 REPGEAEHVKA-VRSGGIPIVHETMEPGAAYCVKATPYKALGXYSASFQTECEVQGEA 230  
 DB 179 ELKNATKRVKQETFTLPVPIGVR-----KFCVKALPRLESHINRKAEMSEECCLITTTBO 232  
 QY 231 I-----PLVLAFAFGFMLILVVPPLFVWKMGRLQYSCCPVVL----- 271  
 DB 233 YFTYTNLSILVISMILFGC-ILVCLVLYOWYIRHPKRL-----PVLVYKRRHDPFPANP 285  
 QY 272 ----PDTLKITN 279  
 DB 286 LCPETPDALHIYD 298

RESULT 12  
 TF\_CAVPO STANDARD; PRT; 289 AA.  
 AC 09JUL8;  
 DT 01-OCT-2000 (Rel. 40, Created)  
 DT 01-OCT-2000 (Rel. 40, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).  
 GN F3.  
 OS Cavia porcellus (Guinea pig).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Hystriognathii; Caviidae; Cavia.  
 OX NCBI\_TaxID=10141;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC TISSUE-Lung;  
 RX MEDLINE=20206020; PubMed=10744153;  
 RA Shi R.J., Li W.Z., Marder V.J., Sporn L.A.;  
 RT Cloning of guinea pig tissue factor cDNA: comparison of primary  
 RT structure among six mammalian species.";  
 RL Thromb. Haemost. 83:455-461(2000).  
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF:VIIA] COMPLEX ACTIVATES  
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN  
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.  
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 CC  
 DR EMBL; AF131949; AAP36523.1; -  
 DR InterPro; IPR001187; -  
 DR Pfam; PF01108; Tissue\_fac1.  
 DR PRINTS; PR00346; TISSUEFACTOR.  
 DR PROSITE; PS00621; TISSUE\_FACTOR.  
 KW Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
 KW Palmitate.  
 FT SIGNAL 1 32  
 FT CHAIN 33 289  
 FT DOMAIN 33 247  
 FT TRANSMEM 248 268  
 FT DOMAIN 269 289  
 FT SITE 44 46  
 FT SITE 75 77  
 FT CARBOHYD 41 41  
 FT CARBOHYD 111 111  
 FT CARBOHYD 151 151  
 FT CARBOHYD 164 164  
 FT DISULFID 79 87  
 FT DISULFID 213 236  
 FT LIPID 271 271  
 SQ SEQUENCE 289 AA; 32456 MW; 7AB97F8F5819F81 CRC64;

Query Match 7.5%; Score 121.5; DB 1; Length 289;  
 Best Local Similarity 24.4%; Pred. No. 0.0011;  
 Matches 69; Conservative 35; Mismatches 98; Indels 81; Gaps 16;

QY 22 ALRPLCLTDEVALLPRA-----PQNLVSLSTNMKHLMSPVLAAGEVYYSVYQGE 73  
 DB 15 AAVPTLLLGWLVQVAAGSIPKVPYPLTWKSTFKILTEMEP--KPINNV-YVQVISTA 71  
 QY 74 YESLYTSIWIPISSWCSLTGEPEDVTDITAVV--PYNLVRATLSSQTSAMSILKHPF 131  
 DB 72 LED-----W-KSICSTIATECDLSEMAPNQYTLARVLSLPRNST---GFLEDAV 120  
 QY 132 NRNS-----TLTRPGMEIKK-XGFHLVIELED-----LGPQFEF 165  
 DB 121 YSNSPEFTPYQETNLGPKIESFELVGTKLNVYRDTOLARSNGTFLSLRDIPKMLQY 180  
 QY 166 LVAYMKREPGEAEHVKA-VRSGGIPIVHETMEPGAAYCVKATPYKAL-----GXYSAFS 219  
 DB 181 MLVYV-RSSTYGRKTAATNTNEF---LIDVQGDGYCF---FVQAVIPSRKDKKSPES 232  
 QY 220 QTECV-----EVOGEALPVLVLAFAFGFMLILVVPVLEF 254



DB 233 IIVCTRLKCKFKREMSRIVVPL-----VIIIVIALFL 266

RESULT 13  
INGR. HUMAN STANDARD; PRT; 489 AA.  
AC P15260;  
DT 01-APR-1990 (Rel. 14, Created)  
DT 01-APR-1990 (Rel. 14, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE INTERFERON-GAMMA RECEPTOR ALPHA CHAIN PRECURSOR (CDW119).  
GN IFNGR1.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP MEDLINE=69003065; PubMed=2971451;  
RT Aguet M., Dembic Z., Merlin G.;  
RL "Molecular cloning and expression of the human interferon-gamma  
receptor.";  
RN [2]  
RP DISULFIDE BONDS, PARTIAL SEQUENCE, AND MUTAGENESIS.  
RN MEDLINE=93183911; PubMed=8443182;  
RT Stueber D., Friedlein A., Fountoulakis M., Lahm H.-W., Garotta G.;  
RL "Alignment of disulfide bonds of the extracellular domain of the  
interferon gamma receptor and investigation of their role in  
biological activity.";  
RN [3]  
RP Biochemistry 32:2423-2430(1993).  
RN [4]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF 26-248.  
RN MEDLINE=95342235; PubMed=7617032;  
RT Walter M.R., Windsor W.T., Nagabushan T.L., Lundell D.J., Lunn C.A.,  
RA Zaodny P.J., Narula S.K.;  
RL "Crystal structure of a complex between interferon-gamma and its  
soluble high-affinity receptor.";  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.8 ANGSTROMS) OF 28-122 COMPLEX WITH ANTIBODY.  
RN MEDLINE=98035727; PubMed=9367779;  
RT Sogabe S., Stuart F., Henke C., Bridges A., Williams G., Birch A.,  
RA Winkler F.K., Robinson U.A.;  
RL "Neutralizing epitopes on the extracellular interferon gamma receptor  
(IFNgammaR) alpha-chain characterized by homolog scanning mutagenesis  
and x-ray crystal structure of the A6 fab-IFNgammaR1-108 complex.";  
RN [5]  
RP J. Mol. Biol. 273:882-897(1997).  
RN [5]  
RP X-RAY CRYSTALLOGRAPHY (2.9 ANGSTROMS) OF COMPLEX WITH ING.  
RN PubMed=10986460;  
RA Thiel D.J., le Du M.-H., Walter R.L., D'Arcy A., Chene C.,  
RA Fountoulakis M., Garotta G., Winkler F.K., Falick S.E.;  
RL "Observation of an unexpected third receptor molecule in the crystal  
structure of human interferon-gamma receptor complex.";  
RN [5]  
RP Structure 8:927-936(2000).  
RN [5]  
RP -1- FUNCTION: RECEPTOR FOR INTERFERON GAMMA. TWO RECEPTORS BIND ONE  
INTERFERON-GAMMA DIMER.  
CC -1- SUBUNIT: MONOMER.  
CC -1- PTM: PHOSPHORYLATED AT SER/THR RESIDUES.  
CC -1- SIMILARITY: CONTAINS 2 IMMUNOGLOBULIN-LIKE C2-TYPE DOMAINS.  
CC -1- SIMILARITY: CONTAINS 2 FIBRINOGEN TYPE III-LIKE DOMAINS.  
CC -1- SIMILARITY: BELONGS TO THE CLASS II CYTOKINE FAMILY OF RECEPTORS.  
CC -1- DATABASE: NAME=PRO; NOTE=CD guide CDW119 entry;  
CC WWW=http://www.ncbi.nlm.nih.gov/ncbi/cd/cdw119.htm.  
CC -----  
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CC -----  
CC EMBL: J03143; AAA52731.1; -  
CC PIR: A31555; A31555.  
CC DR PDB: 1JRH: 25-MAR-98.  
CC DR PDB: 1FC9: 11-AUG-00.  
CC DR Glycositedb: P15260; -  
CC DR MIM: 107470; -  
CC DR MIM: 209950; -  
CC KW Receptor; Transmembrane; Glycoprotein; Signal; Phosphorylation;  
RN Immunoglobulin domain; 3d-structure.  
RN SIGNAL 1 17  
FT CHAIN 18 489 INTERFERON-GAMMA RECEPTOR ALPHA CHAIN.  
FT DOMAIN 18 245 EXTRACELLULAR (POTENTIAL).  
FT TRANSSEM 246 266 POTENTIAL.  
FT DOMAIN 267 489 CYTOPLASMIC (POTENTIAL).  
FT DISULFID 77 85  
FT DISULFID 122 167  
FT DISULFID 195 200  
FT DISULFID 214 235  
FT CARBOHYD 34 34 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 79 79 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 86 86 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 179 179 N-LINKED (GLCNAC. . .) (POTENTIAL).  
FT CARBOHYD 240 240 N-LINKED (GLCNAC. . .) (POTENTIAL).  
SQ SEQUENCE 489 AA; 54404 MW; DCF9E574DBF47400 CRC64;  
Query Match 7.4%; Score 121; DB 1; Length 489;  
Best Local Similarity 21.6%; Pred. No. 0.0022;  
Matches 61; Conservative 54; Mismatches 10; Indels 66; Gaps 13;  
QY 35 LPAPNLVSLTNMKHLMSPVIAGETVY-----YSVEYGEYESLYTSHWIPSSW 88  
DB 29 VPTPTNVITSESNMNPVYWEQIMQVPEVVEKKNQVCK-----NSEMIDA-- 76  
QY 89 CSLTEGPCEDVTDITAVPYN---LRYRAITGSGTSMSILKHPNRRSTLTTPGMEI 145  
DB 77 GINSHHYCNISDHVGD--PSNSLWRYVARVQKESAYAKSEEPVACRDGKIGPKLDI 134  
QY 146 KXGPHLYTEL-----EDLGPQFE-FLVAY--WKEPQAEHYVMVNSG--- 186  
DB 135 RKEKQIMIDIFHPSPVFNQDEQVDYDEPTTCYIRVAVYRAMGSELYQYKILQKEND 194  
QY 187 -----GIVNLETPMGAAYCYKAGTFVRAIGYSAFSQTECEVQGEA-----IP 232  
DB 195 CDEIQCOLAIPV-----SSINSQYCSASAEGLVHMVGVTTEKSKREVCITFNSSIKGSLMIP 250  
QY 233 LVLAFAVGFMLLVVPLFVWKMGRLLQYSCCPVVPDIL 275  
DB 251 VVAALLFL--VLSLVFCFYIKINPLKEKS---IILPKSL 287  
RESULT 14  
TF\_MOUSE STANDARD; PRT; 294 AA.  
AC P20352;  
DT 01-FEB-1991 (Rel. 17, Created)  
DT 01-AUG-1991 (Rel. 19, Last sequence update)  
DT 01-OCT-2000 (Rel. 40, Last annotation update)  
DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).  
GN F3 OR CF3 OR CF-3.  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
OX NCBI\_TaxID=10090;  
RN [1]  
RN SEQUENCE FROM N.A.  
RP MEDLINE=91093171; PubMed=1985911;  
RA Ranganathan G., Blatti S.P., Subramaniam M., Fass D.N., Mahle N.J.,  
RA Getz M.J.;  
RL "Cloning of murine tissue factor and regulation of gene expression by  
transforming growth factor type beta 1.";



RL J. Biol. Chem. 266:496-501(1991).  
 RN [2]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN-BALB/C;  
 RX MEDLINE=89343974; PubMed=2761539;  
 RA Hartzell S., Ryder K., Ianahan A., Iau L.F., Mathans D.,  
 RT "A growth factor-responsive gene of murine BALB/c 3T3 cells encodes a  
 RL protein homologous to human tissue factor".  
 RL Mol. Cell. Biol. 9:2567-2573(1989).  
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES  
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN  
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.  
 CC  
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 CC  
 CC EMBL; M57896; AAA63400.1; -;  
 CC EMBL; M26071; AAA40414.1; -;  
 CC PIR; A32318; KEMS3.  
 CC HSSP; P13726; ITRH.  
 CC MGD; MGI:88381; F3.  
 CC InterPro; IPR001187; -;  
 CC Pfam; PF01108; Tissue\_fac; 1.  
 CC PRINTS; PR00346; TISSUEFACTOR.  
 CC PROSITE; PS00621; TISSUE\_FACTOR; 1.  
 CC Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
 CC Palmitate.  
 CC FT SIGNAL 1 28  
 CC FT CHAIN 29 294  
 CC FT DOMAIN 29 251  
 CC FT TRANSMEM 252 274  
 CC FT DOMAIN 275 294  
 CC FT SITE 245 247  
 CC FT CARBOHYD 37 37  
 CC FT CARBOHYD 57 57  
 CC FT CARBOHYD 169 169  
 CC FT CARBOHYD 200 200  
 CC FT DISULFID 75 83  
 CC FT DISULFID 218 241  
 CC FT LIPID 275 275  
 CC CONFLICT 26 26  
 CC SEQUENCE 294 AA; 32935 MW; A306101293C31FA0 CRC64;

Query Match 7.3%; Score 119.5; DB 1; Length 294;  
 Best Local Similarity 23.3%; Pred. No. 0.0017;  
 Matches 74; Conservative 39; Mismatches 115; Indels 89; Gaps 17;

QY 22 ALIP-----CLTDEVAIIIPAPD---NLSTLSTNMKHLMSVIAIGETVY-YSEVYQGE 73  
 DB 12 ALAPFLCLCLQVYAGAGIPEKAFNLWISTDFKTIEMQ---PKPTNYTYTQDISDR 67  
 QY 74 YESLTSHTWIPSSWCSLTGSEPCVDTDIT--ATVPYNLARATL-----GSG--- 120  
 DB 68 -----SRNM--KNKCESTTDECDLTDEIVADVWYAEAKLVSPRRNSVHGSGQQLVI 119  
 QY 121 -----TSAMSLKHPNRNSTILTRPGME-----IKKXGFHLVI 154  
 DB 120 HGEPPFTNAPKFLPY-----RDTNIGQPIYIQFEDGDKRLNVVYDSLTVKKNGFELTL 175  
 QY 155 ELEDIGPQFEFLVAV--WMREPGAEEHVAKVNRSGIIPVHLETPGAAVC--VKAQTFVKA 211  
 DB 176 R-QVGGKDLGYITTYRKSSGKTKNTINTNTEFSIDV-----EEGVSCVCFQVAMIFSRK 229

QY 212 IGYNSAFSOTECVE---VOGEAIPLYLAFATVGMILLIVVPLPYWKNGLQYSCCP 267  
 DB 230 TGNSSGSSSTVCWEQKSPFGEITLIVGANVLLATIFILLISLCKRRKRRRAGQ----- 284  
 QY 268 VVVLPTLKITKTNPSOKL 284  
 DB 285 -----KGNKTPSRLL 293

RESULT 15  
 TF\_BOVIN  
 ID TF\_BOVIN STANDARD; PRT; 292 AA.  
 AC P30931;  
 DT 01-JUL-1993 (Rel. 26, Created)  
 DT 01-JUL-1993 (Rel. 26, Last sequence update)  
 DT 01-OCT-2000 (Rel. 40, Last annotation update)  
 DE TISSUE FACTOR PRECURSOR (TF) (COAGULATION FACTOR III).  
 GN F3.  
 OS Bos taurus (Bovine).  
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;  
 OC Bovidae; Bovinae; Bos.  
 OX NCBI\_TaxID=9913;  
 RN [1]  
 RP SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.  
 RC TISSUE-Adrenal gland;  
 RX MEDLINE=92109720; PubMed=1764065;  
 RA Takayanoki Y., Muta T., Miyata T., Iwanaga S.,  
 RT Biochem. Biophys. Res. Commun. 181:1145-1150(1991).  
 CC -1- FUNCTION: INITIATES BLOOD COAGULATION BY FORMING A COMPLEX WITH  
 CC CIRCULATING FACTOR VII OR VIIA. THE [TF-VIIA] COMPLEX ACTIVATES  
 CC FACTORS IX OR X BY SPECIFIC LIMITED PROTEOLYSIS. TF PLAYS A ROLE IN  
 CC NORMAL HEMOSTASIS BY INITIATING THE CELL-SURFACE ASSEMBLY AND  
 CC PROPAGATION OF THE COAGULATION PROTEASE CASCADE.  
 CC -1- SUBCELLULAR LOCATION: TYPE I MEMBRANE PROTEIN.  
 CC -1- SIMILARITY: BELONGS TO THE TISSUE FACTOR FAMILY.  
 CC  
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 CC  
 CC EMBL; S74147; AAB20755.1; -;  
 CC PIR; JQ1319; KEB03.  
 CC HSSP; P24055; IAA21.  
 CC InterPro; IPR001187; -;  
 CC Pfam; PR001108; Tissue\_fac; 1.  
 CC PRINTS; PR00346; TISSUEFACTOR.  
 CC PROSITE; PS00621; TISSUE\_FACTOR; 1.  
 CC Glycoprotein; Blood coagulation; Transmembrane; Signal; Lipoprotein;  
 CC Palmitate.  
 CC FT SIGNAL 1 35  
 CC FT CHAIN 36 292  
 CC FT DOMAIN 36 248  
 CC FT TRANSMEM 249 271  
 CC FT DOMAIN 272 292  
 CC FT SITE 46 48  
 CC FT CARBOHYD 43 43  
 CC FT CARBOHYD 153 153  
 CC FT CARBOHYD 181 181  
 CC FT DISULFID 81 89  
 CC FT DISULFID 215 238  
 CC FT LIPID 274 274  
 CC SEQUENCE 292 AA; 32475 MW; 5E471092BFBCE163 CRC64;

Query Match 7.0%; Score 114.5; DB 1; Length 292;  
 Best Local Similarity 19.8%; Pred. No. 0.0046;  
 Matches 49; Conservative 39; Mismatches 103; Indels 57; Gaps 9;

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OY 40 NLSVLTNNMKHLLMSPVIAIGETVYYSVEYQGEYSLTSHI-----WIPSSMCSLFE 93
Db 43 NITWKTNEKFTILEMEP-----KPINHVTVOISPRLGNN--KNKCFYTT 85
OY 94 GPECDDYDDITATVAPYMLRVARATLGSQTSAMSILKHPENRN-----STILTRPGE-I 145
Db 86 NTEGCVTDEIVKKNVRETYLARVLSTYPADTSSSYVEPPPTNSPEFTPYLETNVLGQPTIOSF 145
OY 146 KXKGPHLVIELED-----LGPOFEFLVAYMXRPGAEHEHVKMVRSGGI 188
Db 146 EOYGTKLNTVYQDARTLVBRANSAPLRLDYVGKDLNLTLYYWKASSTGKKKATNTNG-- 203
OY 189 PVHLEMEPGAAYCVKAQTFV--KAIGKXSAFSQTECVVOGEAIPVYLAIPAFVGEMLI 246
Db 204 --FLIDVDKGENYCFHVQAVILSRVNOKSPESPICKTSHEK---VLSTELFLIIGTYML 258
OY 247 LVVVVPLFV 254
Db 259 VIIIFIVV 266

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Search completed: October 12, 2001, 16:11:25  
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